



1

SEQUENCE LISTING

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<120> Omega-Conopeptides

<130> 2314-241

<150> US 60/219,616

<151> 2000-07-21

<150> US 60/265,888

<151> 2001-02-05

<160> 413

<170> PatentIn version 3.0

<210> 1

<211> 318

<212> DNA

<213> Unknown

<220>

<223> unknown Conus species

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aatttctcca cgttgactcg tcgctgcctt tctcccggat cacgatgtca taagacaatg 180

cgtaactgct gcacttcacg ctcttcatac aaagggaaat gtcggcctcg aaaatgaacc 240

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<210> 2

<211> 76

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<400> 2

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1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
20 25 30

Ala Leu Arg Ser Thr Thr Asn Phe Ser Thr Leu Thr Arg Arg Cys Leu

35 40 45
 Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys Thr Ser
 50 55 60

Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
 65 70 75

<210> 3
 <211> 30
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<220>
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 <222> (1)..(30)
 <223> Xaa at residue 4 and 28 is Pro or Hyp; Xaa at residue 22 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 3
 Cys Leu Ser Xaa Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
 1 5 10 15

Thr Ser Cys Ser Ser Xaa Lys Gly Lys Cys Arg Xaa Arg Lys
 20 25 30

<210> 4
 <211> 283
 <212> DNA
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 4
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 aatttctcca cgtcgactcg tcgctgcaaa cctcccggaa gaaaatgtct gaatagaaag 180
 aatgaatgct gcagcaagtt ttgcaatgaa cacctacata tgtgtggata aatggctaaa 240
 aactgaataa aagccgcatt gcaaaaaaaaaa aaaaaaaaaa aaa 283

<210> 5
 <211> 74
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 5
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 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His His
 20 25 30

Phe Cys Asn Glu His Leu His Met Cys Gly
65 70

<210>	6
<211>	27
<212>	PRT
<213>	Unknown

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<220>
<223> unknown Conus species
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<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 14 and 22 is Glu or gamma-carboxy Glu; Xaa at resi
      due 3 and 4 is Pro or Hyp
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<400> 6
Cys Lys Xaa Xaa Gly Arg Lys Cys Leu Asn Arg Lys Asn Xaa Cys Cys
1 5 10 15

Ser Lys Phe Cys Asn Xaa His Leu His Met Cys
20 25

<210>	7
<211>	275
<212>	DNA
<213>	Unknown

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<220>
<223> unknown Conus species
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aatctctcca tatcgtctcg ctgcaaacct cccagaagaa aatgtctgaa gattaaggat      180
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ataaaagccg cattgcaaaa aaaaaaaaaa aaaaaa      275
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<210>	8
<211>	72
<212>	PRT
<213>	Unknown

<220>
<223> unknown Conus species

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<400> 8
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
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Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met Gln Lys His Tyr
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Ile Ser Ser Arg Cys Lys Pro
 35 40 45

Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys Asn Phe Cys
 50 55 60

Asn Thr His Leu Asn Met Cys Gly
 65 70

<210> 9
 <211> 26
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<220>
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 <223> Xaa at residue 3 and 4 is Pro or Hyp

<400> 9
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 1 5 10 15

Asn Phe Cys Asn Thr His Leu Asn Met Cys
 20 25

<210> 10
 <211> 377
 <212> DNA
 <213> Unknown

<220>
 <223> unknown Conus species

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 aaactctcca tgtcgactcg ctgcgaggt ccaggaacaa tttgtcctaa tagggatatgc 180
 tgcggttatt gcagtaaaaag aacacatcta tgtcattcgc gaactggctg atcttcccc 240
 ttctgcgctc catccttttc tgccctgagtc ctccatacct gagaatggctc atgaaccact 300
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 aaaaaaaaaa aaaaaaa 377

<210> 11
 <211> 74
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 11
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Met Ala
 1 5 10 15

Cys Gln Leu Val Thr Ala Asp Gly Ser Arg Gly Met His Lys His Tyr
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Ser Thr Arg Cys Ala Gly
35 40 45

Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly
65 70

<210> 12

<211> 28

<212> PRT

<213> Unknown

<220>

<223> unknown Conus species

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
r

<400> 12

Cys Ala Gly Xaa Gly Thr Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
20 25

<210> 13

<211> 323

<212> DNA

<213> Conus arenatus

<400> 13

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ctcattacag gtgagcagaa ggacatgct ctgagggtcaa ctgacaaaaa ctccaagttg 120

actaggcagt gctcggctaa cggtggatct tgtactcgtc attttcactg ctgcagcctc 180

tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240

ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300

caataaaaaa aaaaaaaaaa aaa 323

<210> 14

<211> 73

<212> PRT

<213> Conus arenatus

<400> 14

Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
 35 40 45

Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
 50 55 60

Ser Val Cys Val Ala Thr Ser Tyr Pro
 65 70

<210> 15
 <211> 33
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or
 Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 -iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 15
 Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 16
 <211> 326
 <212> DNA
 <213> Conus arenatus

<400> 16
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 ctgaggtcaa ctgacagaaa ctccaagttg accaggacat gcaacactcc cactgaatat 180
 tgtactttgc atcgacactg ctgcagcggc tactgccata aaacaatcca ggcatgttca 240
 taataccggt gagtgggtcat gaaccactca ataccctctc ctctggaggc ttcagaggaa 300
 ctgcattgaa ataaaagccg cattgc 326

<210> 17
 <211> 74
 <212> PRT
 <213> Conus arenatus

<400> 17
 Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
 20 25 30

His Ala Leu Arg Ser Thr Asp Arg Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys Ser Gly

50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
65 70

<210> 18
<211> 28
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is
Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 18
Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Arg His Cys Cys
1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
20 25

<210> 19
<211> 332
<212> DNA
<213> Conus arenatus

<400> 19
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ctgagggtcaa ctgacaaaaa ctccaagttg actaggcagt gcacgcctaa cggtggatct 180
tgttctcgtc attttcactg ctgcagcctc tattgcaata aaagtactgg cgtatgtatt 240
gcaacctcat acccgtgagt ggtcatgaac cactcaatac cctctcctct ggaggcttca 300
gaggaactgc attgaaataa aagccgcatt gc 332

<210> 20
<211> 79
<212> PRT
<213> Conus arenatus

<400> 20
Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
35 40 45

Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
50 55 60

Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr Pro
65 70 75

<210> 21

<211> 33
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 33 is P
 ro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-T
 yr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21
 Xaa Cys Thr Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Xaa Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 22
 <211> 332
 <212> DNA
 <213> Conus arenatus

<400> 22
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 gacaaaaact ccaagttgac caggacatgc aacactccca ccgaatattg tactttgcat 180
 caacactgct gcagcggcta ctgccataaa acaatccagg catgttcata ataccggtga 240
 gtgggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
 aaaaccgcat tacaaaaaaa aaaaaaaaaa aa 332

<210> 23
 <211> 74
 <212> PRT
 <213> Conus arenatus

<400> 23
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Lys His
 20 25 30

His Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
 35 40 45

Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
 50 55 60

Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
 65 70

<210> 24
 <211> 28
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is
 Pro or Hyp; Xaa at residue 8 and 19 is Tyr, 125I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 24
 Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys
 1 5 10 15

Ser Gly Xaa Cys His Lys Thr Ile Gln Ala Cys Ser
 20 25

<210> 25
 <211> 394
 <212> DNA
 <213> Conus arenatus

<400> 25
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 ctcattacag ctgagactta ctccagaggt aagcagatgc accgcgctct gaggtcaact 120
 gacaaaaact cccagttgac caggggaatgc acacctcccg gtggagcttg tggtttacct 180
 acacactgct gcgggttttg cgatactgca aacaacagat gtctgtaaag ctgggtctggc 240
 gtctgatatt ccccttctgt gctctatcct ctttggcctg agtcatccgt acctgtgagt 300
 ggtcatgaac tactcaatac cctctcctct ggaggcttca gaggaactac aatgaaataa 360
 aaccgcgatt gcagagaaaa aaaaaaaaaa aaaa 394

<210> 26
 <211> 73
 <212> PRT
 <213> Conus arenatus

<400> 26
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
 35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
 50 55 60

Cys Asp Thr Ala Asn Asn Arg Cys Leu
 65 70

<210> 27
 <211> 27
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5

and 12 is Pro or Hyp

<400> 27
Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
20 25

<210> 28
<211> 345
<212> DNA
<213> Conus arenatus

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<221> misc_feature
<222> (1)..(345)
<223> n may be any nucleotide

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gacaaaaact ccaagttgac caggacatgc aacactccca ctgaatattg tactttgcat 180
caacactgct gcagcggcca ctgccataaa acaatccagg catgtgcata ataccggtgg 240
gtggtcatga accactcaat accctctcct ctggaggctt cagaggaact gcattgaaat 300
aaaaccgcat tgcaatgaan aaaaaaaaaa aaaaaaaaaa aaaaaa 345

<210> 29
<211> 74
<212> PRT
<213> Conus arenatus

<400> 29
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Glu Gln Asn His
20 25 30
His Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Thr Cys
35 40 45
Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys Ser Gly
50 55 60
His Cys His Lys Thr Ile Gln Ala Cys Ala
65 70

<210> 30
<211> 28
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 5 is
Pro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 30

Thr Cys Asn Thr Xaa Thr Xaa Xaa Cys Thr Leu His Gln His Cys Cys
 1 5 10 15

Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
 20 25

<210> 31

<211> 322

<212> DNA

<213> Conus arenatus

<400> 31

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 actaggcagt gctcgcctat cggtggatat tgtactcttc atattcactg ctgcagcaac 180
 cattgcatta aacctatcgg ccgatgtgtg gcaacctgat acccgtgcgt ggtcatgaac 240
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcattg 300
 caataaaaaa aaaaaaaaaa aa 322

<210> 32

<211> 70

<212> PRT

<213> Conus arenatus

<400> 32

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30

Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Pro Ile Gly Gly Tyr
 35 40 45

Cys Thr Leu His Ile His Cys Cys Ser Asn His Cys Ile Lys Pro Ile
 50 55 60

Gly Arg Cys Val Ala Thr
 65 70

<210> 33

<211> 30

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i
 odo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 33

Xaa Cys Ser Xaa Ile Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
 1 5 10 15

Ser Asn His Cys Ile Lys Xaa Ile Gly Arg Cys Val Ala Thr
 20 25 30

<210> 34
 <211> 318
 <212> DNA
 <213> Conus arenatus

<400> 34
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 ctactacag gtgagcagaa ggacccatgct ctgagggtcaa ctgacaaaaa ctccaagttg 120
 actaggcagt gcttgcctaa cggtggatat tgtactcttc atattcactg ctgcagcgac 180
 cattgcatta aacctatcga ccgatgtgtg gcaacctgat acccggggcgt ggtcatgaac 240
 cctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300
 caaaaaaaaa aaaaaaaaaa 318

<210> 35
 <211> 70
 <212> PRT
 <213> Conus arenatus

<400> 35
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Leu Pro Asn Gly Gly Tyr
 35 40 45
 Cys Thr Leu His Ile His Cys Cys Ser Asp His Cys Ile Lys Pro Ile
 50 55 60
 Asp Arg Cys Val Ala Thr
 65 70

<210> 36
 <211> 30
 <212> PRT
 <213> Conus arenatus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 and 23 is P
 ro or Hyp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-i
 odo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 36
 Xaa Cys Leu Xaa Asn Gly Gly Xaa Cys Thr Leu His Ile His Cys Cys
 1 5 10 15
 Ser Asp His Cys Ile Lys Xaa Ile Asp Arg Cys Val Ala Thr
 20 25 30

<210> 37
 <211> 374
 <212> DNA
 <213> Conus aurisiacus

<400> 37

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atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcatc      60
acagctgatg actccagagg tacgcagaag catcgttccc tgagctcggc caccaaactc      120
tccatgtcga ctcgctgcaa gggtaaagga aaaccatgca gtaggatttc gtataactgc      180
tgcaccgggtt cttgcagatc aggtaaagtgt ggctgatcca gcgcctgata ttcccccttc      240
tgtgctctat ccttttctgc ctgagtcctc cttacctgag agtgggtcatg aaccactcat      300
cacctgctcc tctggaggcc ccagaggagc tacattgaaa taaaagtcgc attgcaaaaa      360
aaaaaaaaaa aaaa                                                         374

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<210> 38
<211> 71
<212> PRT
<213> Conus aurisiacus

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<400> 38
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
          35          40          45
Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys Thr Gly Ser
          50          55          60
Cys Arg Ser Gly Lys Cys Gly
65          70

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<210> 39
<211> 25
<212> PRT
<213> Conus aurisiacus

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<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr,
      mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 39
Cys Lys Gly Lys Gly Lys Xaa Cys Ser Arg Ile Ser Xaa Asn Cys Cys
1          5          10          15
Thr Gly Ser Cys Arg Ser Gly Lys Cys
          20          25

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<210> 40
<211> 380
<212> DNA
<213> Conus aurisiacus

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<400> 40
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acagctgatg actccagagg tacgcagaag catcgttccc tgaggtcgaa gaccaaactc      120
tccatgtcga ctggctgcat ggaagccgga tcttattgcg gctctactac gagaatctgc      180

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tgcgggttttt gcgcttattt cggcaaaaaa tgtattgact atcccagcaa ctgatcttcc 240
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 actcatcacc tgctcctctg gagggcccag aggagctaca ttgaaataaa atcgcatcgc 360
 taaaaaaaaa aaaaaaaaaa 380

<210> 41
 <211> 77
 <212> PRT
 <213> Conus aurisiacus

<400> 41
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ser Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Gly Cys Met Glu
 35 40 45
 Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys Gly Phe Cys
 50 55 60
 Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
 65 70 75

<210> 42
 <211> 32
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(32)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 30 is
 s Pro or Hyp; Xaa at residue 7, 21 and 29 is Tyr, 125I-Tyr, mono-
 iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 42
 Cys Met Xaa Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg Ile Cys Cys
 1 5 10 15
 Gly Phe Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa Xaa Ser Asn
 20 25 30

<210> 43
 <211> 373
 <212> DNA
 <213> Conus aurisiacus

<400> 43
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccttg 120
 agctcggcca ccaaactctc catgtcgact cgctgcaagg cttaaaggaaa accatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gttaaagtgg ctgatccagt 240
 gcctgatctt ccccttctg tgctctatcc ttttctgcct gagtcctcct tacctgagag 300

tggatcatgaa ccactcatca cctgctcctc tggaggcccc agaggagcta cattgaaata 360
 aaagccgcat tgc 373

<210> 44
 <211> 71
 <212> PRT
 <213> Conus aurisiacus

<400> 44
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ser Leu Ser Ser Ala Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
 35 40 45

Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 45
 <211> 25
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr,
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 45
 Cys Lys Ala Lys Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 46
 <211> 379
 <212> DNA
 <213> Conus aurisiacus

<400> 46
 accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcgaaga caaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180
 ggtattgaca acgactgctg caatgcatgc gatccaggaa gaaatatatg tacgtagctg 240
 atccagcgcc tgatcttccc ccttctgtgc tctatccttt tctgcccagag tcctccttac 300
 ctgagagtgg tcatgaacca ctcacacct gctccctgga ggcctcagag gagctacaat 360
 gaaataaaaag ccgcattgc 379

<210> 47

<211> 72
 <212> PRT
 <213> Conus aurisiacus

<400> 47
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
~~Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys~~
~~50 55 60~~

Asp Pro Gly Arg Asn Ile Cys Thr
 65 70

<210> 48
 <211> 26
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
 r

<400> 48
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Xaa Gly Arg Asn Ile Cys Thr
 20 25

<210> 49
 <211> 382
 <212> DNA
 <213> Conus bullatus

<400> 49
 accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcagagca tcttgccctg 120
 aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgcgga 180
 cctgctacta cgaaaatctg ctgcatgttt tgcagtcctat tcagcgatag atgtatgaac 240
 aatcccaaca attgatcttc ccccttgtgt gctccatcct tttctgcctg agtcctcctt 300
 acctgagagt ggtcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360
 attgaaataa aagccgcatt gc 382

<210> 50
 <211> 78
 <212> PRT
 <213> Conus bullatus

<400> 50
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45
 Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
 50 55 60
 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
 65 70 75

<210> 51
 <211> 36
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono
 -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 51
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30
 Asn Xaa Asn Asn
 35

<210> 52
 <211> 400
 <212> DNA
 <213> Conus bullatus

<400> 52
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaacaccc tgtgtcgact cgctgcatta ctccaggaac acgatgtaag 180
 gttccgagcc aatgctgcag aggtccttgc aagaacggtc gttgtactcc atccccttct 240
 gaatggtaaa tgtggttgat ccagcgctg atcttcccc ttcgtcgtgc tccatccttt 300
 tctgcctgag tctccttac ctgagagtgg tcatgaacca ctcatcacct actcccctgg 360
 aggcttcaga ggagctacat tgaaataaaa gccgcattgc 400

<210> 53
 <211> 76
 <212> PRT
 <213> Conus bullatus

<400> 53

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
20 25 30

Ala Leu Arg Lys Ala Thr Lys His Pro Val Ser Thr Arg Cys Ile Thr
35 40 45

Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Gly Pro Cys
50 55 60

Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp
65 70 75

<210> 54

<211> 31

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residue 30 is Glu or gamma-carboxy Glu; Xaa at residue 4,
11, 18, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo
Trp

<400> 54

Cys Ile Thr Xaa Gly Thr Ala Cys Lys Val Xaa Ser Gln Cys Cys Arg
1 5 10 15

Gly Xaa Cys Lys Asn Gly Arg Cys Thr Xaa Ser Xaa Ser Xaa Xaa
20 25 30

<210> 55

<211> 379

<212> DNA

<213> Conus bullatus

<400> 55

acaaaaacca tcatcaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcattac agctgaggac tccagagata cgcagaagca tcgtgccctg 120

aggtcggaca ccaaactctc catgttgact ttgcgctgcg caacttacgg aaaaccttgt 180

ggtattcaaa acgactgctg caatacatgc gatccagcca gaaggacatg tacgtagctg 240

atccggcgtc ttgatcctcc gcttctgtgc tccatctttt ctgcctgagt cctccttacc 300

tgagagtggc catgaaccac tcatcaccta ctctctgga ggctttagag gagctacatt 360

gaaataaaaag ccgcattgc 379

<210> 56

<211> 72

<212> PRT

<213> Conus bullatus

<400> 56

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Asp Thr Gln Lys His Arg

20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
35 40 45

Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn Thr Cys
50 55 60

Asp Pro Ala Arg Arg Thr Cys Thr
65 70

<210> 57

<211> 26

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
r

<400> 57

Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
1 5 10 15

Thr Cys Asp Xaa Ala Arg Arg Thr Cys Thr
20 25

<210> 58

<211> 373

<212> DNA

<213> Conus bullatus

<400> 58

accaaaacca tcatacaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg 60

acggcctgtc agctcattac agctgaagac tccagaggta cgcagttgca tcgtgccctg 120

aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc atcatgtata 180

aggattgcgt ataactgctg caagtattct tgcagaaatg gtaaattgtg ctgatccagc 240

gcctgatctt ccccttgtg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300

tggtcatgaa ccaatcatca cctactcctc tggaggcttc agaggagcta cattgaaata 360

aaagccgcat tgc 373

<210> 59

<211> 71

<212> PRT

<213> Conus bullatus

<400> 59

Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
35 40 45

Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
 50 55 60

Cys Arg Asn Gly Lys Cys Gly
 65 70

<210> 60
 <211> 25
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 60
 Cys Lys Gly Xaa Gly Ala Ser Cys Ile Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Lys Xaa Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 61
 <211> 382
 <212> DNA
 <213> Conus bullatus

<400> 61
 atcaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaagac tccagaggta cgcattgagca tcttgccctg 120
 aagtcgacct ccaaagtctc caagtcgact agctgcatgg cagccggatc ttattgcgga 180
 cctgctacta cgaatatctg ctgcatgttt tgcagtcctat tcagcgatag atgtatgaaa 240
 aagcccaaca attgatcttc ccccttctgt gctctatcct tttctgcctg agtcctcctt 300
 acctgagagt ggatcatgaac cactcatcac ctactcctct ggaggcttca gaggagctac 360
 attgaaataa aagccgcatt gc 382

<210> 62
 <211> 78
 <212> PRT
 <213> Conus bullatus

<400> 62
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30

Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Ala
 35 40 45

Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr Asn Ile Cys Cys Asp Phe
 50 55 60

Cys Ser Pro Phe Ser Asp Arg Cys Met Lys Lys Pro Asn Asn

65

70

75

<210> 63
 <211> 36
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue 13, 25 and 34 is Pro or Hyp; Xaa at residue 10 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Tyr

<400> 63

Ser Thr Ser Cys Met Ala Ala Gly Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15

Asn Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Lys
 20 25 30

Lys Xaa Asn Asn
 35

<210> 64
 <211> 373
 <212> DNA
 <213> Conus bullatus

<400> 64

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattat agctgaggac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtaaaggatc atcatgtcat 180
 aggacttcgt atgactgctg cacgggttct tgcagaaatg gtagatgtgg ctgatccagc 240
 gcctgatctt ccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag 300
 tggatcatgaa ccactcatca cctactcctc tggagggttc agaggagcta cattgaaata 360
 aaagccgcat tgc 373

<210> 65
 <211> 71
 <212> PRT
 <213> Conus bullatus

<400> 65

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Ile Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30

Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
 35 40 45

Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Asn Gly Arg Cys Gly
 65 70

<210> 66
 <211> 25
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 66
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Arg Cys
 20 25

<210> 67
 <211> 321
 <212> DNA
 <213> Conus characteristicus

<400> 67
 ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac ggccctgtcaa 60
 ctcattacag gtgagcagaa ggaccatgct ctgagggtcaa ctgacaaaaa ctccaagttg 120
 actaggcagt gctcggctaa cgggtggatct tgtactcgtc attttcactg ctgcagcctc 180
 tattgcaata aagattccag tgtatgtgtg gcaacctcat acccgtgagt ggccatgaac 240
 ccctcaatac cctctcctct ggaggcttca gaggaactgc attgaaataa aaccgcatta 300
 caaaaaaaaa aaaaaaaaaa a 321

<210> 68
 <211> 73
 <212> PRT
 <213> Conus characteristicus

<400> 68
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Gly Glu Gln Lys Asp His Ala Leu Arg Ser Thr
 20 25 30
 Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys Ser Ala Asn Gly Gly Ser
 35 40 45
 Cys Thr Arg His Phe His Cys Cys Ser Leu Tyr Cys Asn Lys Asp Ser
 50 55 60
 Ser Val Cys Val Ala Thr Ser Tyr Pro
 65 70

<210> 69
 <211> 33
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE

<222> (1)..(33)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 33 is Pro or Hyp; Xaa at residue 19 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 69
 Xaa Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15
 Ser Leu Xaa Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Xaa
 20 25 30

Xaa

<210> 70
 <211> 26
 <212> PRT
 <213> Conus catus

<400> 70
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Arg Cys Gly
 20 25

<210> 71
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 71
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Arg Cys
 20 25

<210> 72
 <211> 229
 <212> DNA
 <213> Conus catus

<400> 72
 tcgactcgct gccagggtag aggagcatca tgtcgtaaga ctatgtataa ctgctgcagc 60
 ggttcttgca acagaggtag ttgtggctga tccggcgctt gatcttcccc cttccgtgct 120
 ctatcctttt ctgcctgatt cctccttacc tgagagcggt catgaaccac tcatcacctg 180
 ctccctctgga ggcctcagag gagctacatt gaaataaaaag ccgcattgc 229

<210> 73
 <211> 29
 <212> PRT
 <213> Conus catus

<400> 73

Ser Thr Arg Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr
1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Ser Cys Gly
20 25

<210> 74
<211> 25
<212> PRT
<213> Conus catus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
-sulpho-Tyr or O-phospho-Tyr

<400> 74
Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Ser Cys
20 25

<210> 75
<211> 235
<212> DNA
<213> Conus catus

<400> 75
tcgacacgct gcttgccctgc cggagagtct tgccttttta gtaggattag atgctgcggt 60
acttgcagtt cagtcttaaa gtcattgtgtg agctgatcca gctgctgac ttctctctcc 120
tgtgctccat ccttttctgc ctgagtcctc cttatctgag agtggtcatg aaccactcac 180
cacctactct tctggaggct tcagaggagc tacagtgaag taaaagccgc attgc 235

<210> 76
<211> 31
<212> PRT
<213> Conus catus

<400> 76
Ser Thr Arg Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile
1 5 10 15

Arg Cys Cys Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
20 25 30

<210> 77
<211> 28
<212> PRT
<213> Conus catus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 3 is
Pro or Hyp

<400> 77
Cys Leu Xaa Ala Gly Xaa Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

25

Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
 20 25

<210> 78
 <211> 227
 <212> DNA
 <213> Conus catus

<400> 78
 tcgacacgct gccagggtag aggaggacca tgtactaagg ctgtgttttaa ctgctgcagc 60
 ggttcttgca acagaggtag atgtggctga tccagcgcct gatcttcccc cttctgtgct 120
 ctatcctttt ctgcctgagt cctccttact gagagtagtc atgaaccact catcacctac 180

 tcctctggag gcctcagaga gctacattga aataaaagcc gcattgc 227

<210> 79
 <211> 29
 <212> PRT
 <213> Conus catus

<400> 79
 Ser Thr Arg Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
 20 25

<210> 80
 <211> 25
 <212> PRT
 <213> Conus catus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp

<400> 80
 Cys Gln Gly Arg Gly Gly Xaa Cys Thr Lys Ala Val Phe Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 81
 <211> 236
 <212> DNA
 <213> Conus catus

<400> 81
 ttaactttgc gctgcgcaac ttacggaaaa ccttgtggta ttcaaaacga ctgctgcaat 60
 acatgcgatc cagccagaaa gacatgtacg tagctgatcc ggcgtctgat ctccccctt 120
 ctgtgctcta tccttttctg cctgagtcct ccttacctga gagtgggtcat gaaccactca 180
 tcacctgctc ctctggaggc ctcgggggag ctacattgaa ataaaagccg cattgc 236

<210> 82
 <211> 30
 <212> PRT
 <213> Conus catus

<400> 82

Leu Thr Leu Arg Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn
 1 5 10 15

Asp Cys Cys Asn Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25 30

<210> 83

<211> 26

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
 r

<400> 83

Cys Ala Thr Xaa Gly Lys Xaa Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 84

<211> 229

<212> DNA

<213> Conus catus

<400> 84

tcgactcgct gccggggttag aggaggacca tgtactaagg ctatgttttaa ctgctgcagc 60

ggttcttgca acagaggttag atgtggctga tccagcgcct gatcttcccc cttctgtgct 120

ctatcctttt ctgcctgagt cctccttaac tgagagtagt catgaaccac tcatcaccta 180

ctcctctgga ggcctcagag aagcatcatt gaaataaaag ccgcattgc 229

<210> 85

<211> 29

<212> PRT

<213> Conus catus

<400> 85

Ser Thr Arg Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe
 1 5 10 15

Asn Cys Cys Ser Gly Ser Cys Asn Arg Gly Arg Cys Gly
 20 25

<210> 86

<211> 25

<212> PRT

<213> Conus catus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp

<400> 86

Cys Arg Gly Arg Gly Gly Xaa Cys Thr Lys Ala Met Phe Asn Cys Cys

1 5 10 15

Ser Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 87
<211> 374
<212> DNA
<213> Conus circumcisis

<400> 87
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
aggtcggaca ccaaactccc catgtcgact cgctgcaagg gtaaaggagc atcatgtcgt 180
aagactatgt ataactgctg cagcggttct tgcagcaacg gtagatgtgg ctgatccagc 240
gcctgatctt ccccttctg ctgctctatc cttttctgcc tgagtcctcc ttacctgaga 300
gctggtcatg aaccactcat cacctgctcc tctggaggcc cagaggagct acattgaaat 360
aaaagccgca ttgc 374

<210> 88
<211> 71
<212> PRT
<213> Conus circumcisis

<400> 88
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
20 25 30
Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Gly
35 40 45
Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys Ser Gly Ser
50 55 60
Cys Ser Asn Gly Arg Cys Gly
65 70

<210> 89
<211> 25
<212> PRT
<213> Conus circumcisis

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
-sulpho-Tyr or O-phospho-Tyr

<400> 89
Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Xaa Asn Cys Cys
1 5 10 15
Ser Gly Ser Cys Ser Asn Gly Arg Cys
20 25

<210> 90
 <211> 379
 <212> DNA
 <213> Conus circumciscus

<400> 90
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggcca ccaaagtctc caagtcgact agctgcatgg aagccggatc ttattgccgc 180
 tctactacga gaacctgctg cggttattgc tcttattttca gcaaaaaatg tattgacttt 240
 cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctgagt cctccttacc 300
 tgagagtggg catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 91
 <211> 77
 <212> PRT
 <213> Conus circumciscus

<400> 91
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Ala Thr Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45
 Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
 50 55 60
 Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe Pro Ser Asn
 65 70 75

<210> 92
 <211> 35
 <212> PRT
 <213> Conus circumciscus

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 33 is
 s Pro or Hyp; Xaa at residue 10, 21 and 24 is Tyr, 125I-Tyr, mono-
 -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 92
 Ser Thr Ser Cys Met Xaa Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
 1 5 10 15
 Thr Cys Cys Gly Xaa Cys Ser Xaa Phe Ser Lys Lys Cys Ile Asp Phe
 20 25 30
 Xaa Ser Asn
 35

<210> 93

<211> 379
 <212> DNA
 <213> Conus circumcisis

<400> '93
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
 aggtcggaca ccaaactccc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180
 aggcttatgt atgactgctg cagcggttct tgcagcaggt actcaggtag atgtggctga 240
 tccagcgcct gatcttcccc cttctgctgc tctatccttt tctgcctgag tcctccttac 300
 ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggcccagag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 94
 <211> 73
 <212> PRT
 <213> Conus circumcisis

<400> 94
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Pro Met Ser Thr Arg Cys Lys Ser
 35 40 45
 Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60
 Cys Ser Arg Tyr Ser Gly Arg Cys Gly
 65 70

<210> 95
 <211> 27
 <212> PRT
 <213> Conus circumcisis

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 95
 Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Ser Arg Xaa Ser Gly Arg Cys
 20 25

<210> 96
 <211> 379
 <212> DNA
 <213> Conus circumcisis

<400> 96

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accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg      60
acgacctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccctg      120
acgtcggcca ccaaagtctc caagtcgact ggctgcatga aagccggatc ttattgccgc      180
tctactacga gaacttgctg cggttattgc gcttatttcg gcaaaaaatg tattgactat      240
cccagcaact gatcttcccc ctactgtgct ctatcctttt ctgcctaagt cctccttacc      300
tgagagtggg catgaaccac tcatcaccct actcctctgg aggcccagag gagctacatt      360
gaaataaaag ccgcattgc                                                    379

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<210> 97
<211> 77
<212> PRT
<213> Conus circumcisis

```

```

<400> 97
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
          20          25          30
Ser Leu Thr Ser Ala Thr Lys Val Ser Lys Ser Thr Gly Cys Met Lys
          35          40          45
Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
          50          55          60
Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
65          70          75

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<210> 98
<211> 35
<212> PRT
<213> Conus circumcisis

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<220>
<221> PEPTIDE
<222> (1)..(35)
<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
      phospho-Tyr

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<400> 98
Ser Thr Gly Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
1          5          10          15
Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
          20          25          30
Xaa Ser Asn
          35

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<210> 99
<211> 362
<212> DNA
<213> Conus consors

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<400> 99
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc      60

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acagctgatg actccagagg tacgcagaag catcgtgccc tgaagtctta caccaaactc 120
 tccatgttaa ctttgcgctg cgcatcttac ggaaaacctt gtggtattga caacgactgc 180
 tgcaatacat gcgatccagc cagaaagaca tgtacgtagc tgatccggcg tctgatcttc 240
 ccccttctgt gctctatcct tttctgcctg agtcctcctt acctgagagt ggtcatgaac 300
 cactcatcac ctagctcctc tggaggcttc agaggagcta caatgaaata aaagcgcatc 360
 gc 362

<210> 100
 <211> 72
 <212> PRT
 <213> Conus consors

<400> 100
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Lys Ser Tyr Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Thr Cys
 50 55 60
 Asp Pro Ala Arg Lys Thr Cys Thr
 65 70

<210> 101
 <211> 26
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
 r

<400> 101
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 102
 <211> 237
 <212> DNA
 <213> Conus consors

<400> 102
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcctc 60
 acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgga caccaaactc 120
 tccatgtcga ctcgctgcaa gggtacagga aaaccatgca gtaggattgc gtataactgc 180

tgcaccgggtt cttgcagatc aggtaaatgt ggctgatcca gcgcctgatc tcccccc 237

<210> 103
 <211> 71
 <212> PRT
 <213> Conus consors

<400> 103
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45

Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 104
 <211> 25
 <212> PRT
 <213> Conus consors

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr,
 r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 104
 Cys Lys Gly Arg Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 105
 <211> 320
 <212> DNA
 <213> Conus consors

<400> 105
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60
 acagctgatg actccaaagg tacgcagaag catcggtccc tgaggctgac caccaaagtc 120
 tccaaggcga ctgactgcat tgaagccgga aattattgcg gacctactgt tatgaaaatc 180
 tgctgcggct tttgcagtcc atacagcaaa atatgtatga actatcccca aaattgatct 240
 tcccccttct gtgctctatc cttttctgcc tgagtcctcc ttacctgaga gtgggtcatga 300
 accactcatc acctcgtccc 320

<210> 106
 <211> 78
 <212> PRT
 <213> Conus consors


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<400> 106
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Lys Gly Thr Gln Lys His Arg
          20          25          30
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
          35          40          45
Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
          50          55          60
Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Gln Asn
65          70          75

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<210> 107
<211> 36
<212> PRT
<213> Conus consors

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<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
      25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
      I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 107
Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
1          5          10          15
Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
          20          25          30
Xaa Xaa Gln Asn
          35

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<210> 108
<211> 321
<212> DNA
<213> Conus consors

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<400> 108
atgaaactga cgtgtgtggt gatcgctgcc gtgctgctcc tgacggcctg tcaactcctc      60
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggctcga caccaaactc      120
tccatgtcga ctcgctgcaa aggtaaagga gcatcatgta caaggcttat gtatgactgc      180
tgccacgggt cttgcagcag cagcaagggt agatgtggct gatccggcgc ctgatcttcc      240
cccttctgtg ctctatcctt ttctgcctga gtcctcctta cctgagaggt ggatcatgaac      300
cactcatcac ctgctcccct g                                     321

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<210> 109
<211> 73
<212> PRT
<213> Conus consors

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<400> 109
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15

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Cys Gln Leu Leu Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ala Ser Cys Thr Arg Leu Met Tyr Asp Cys Cys His Gly Ser
50 55 60

Cys Ser Ser Ser Lys Gly Arg Cys Gly
65 70

<210> 110

<211> 27

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 110

Cys Lys Gly Lys Gly Ala Ser Cys Thr Arg Leu Met Xaa Asp Cys Cys
1 5 10 15

His Gly Ser Cys Ser Ser Ser Lys Gly Arg Cys
20 25

<210> 111

<211> 292

<212> DNA

<213> Conus consors

<400> 111

ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggccctgtcaa 60

ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120

aaactctcca tgtcaactcg ctgcaagggt aaaggagcat catgtcatag gacttcgtat 180

gactgctgca ccggttcttg caacagaggt aaatgtggct gatccggcgc ctgatcttcc 240

cccttctgtg ctctatcctt ttctgcctga gtcattcata cctgtgctcg ag 292

<210> 112

<211> 71

<212> PRT

<213> Conus consors

<400> 112

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
50 55 60

Cys Asn Arg Gly Lys Cys Gly
65 70

<210> 113
<211> 25
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 113
Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 114
<211> 299
<212> DNA
<213> Conus consors

<400> 114
ggatccatga aactgacgtg cgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgaa gtcggacacc 120
aaactctcca tgttaacttt gcgctgcgca tcttacggaa aaccttgtgg tatttacaac 180
gactgctgca atacatgcga tccagccaga aagacatgta cgtagctgat ccggcgtctg 240
atcttcccc ttctgtgctc tacccttttc tgctgagtc atccatacct gtgctcgag 299

<210> 115
<211> 72
<212> PRT
<213> Conus consors

<400> 115
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr
65 70

<210> 116
<211> 26
<212> PRT
<213> Conus consors

<220>

<221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
 spho-Tyr

<400> 116
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 117
 <211> 434
 <212> DNA
 <213> Conus consors

<220>
 <221> misc_feature
 <222> (1)..(434)
 <223> n may be any nucleotide

<400> 117
 ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcggacacc 120
 aaactctcca tgtcgactcg ctgcaagggt acaggaaaac catgcagtag ggttgcgtat 180
 aactgctgca ccggttcttg cagatcaggt aaatgtggct gatccagtgc ctgatcttcc 240
 cccttctgtg ctctatcctt ttctgectga gtctctctta cctgagagtg gtcatgaacc 300
 actcatcacc tgctcctctg gaggcttcag aggagctaca ttgaaataaa agccgcattg 360
 cantgnanaa aannnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnggaaaaaa 420
 aaaaaaaaaa aaaa 434

<210> 118
 <211> 71
 <212> PRT
 <213> Conus consors

<400> 118
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60
 Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 119
 <211> 25
 <212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 119

Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Val Ala Xaa Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 120

<211> 393

<212> DNA

<213> Conus consors

<400> 120

```
ggatccatga aactgacgtg catggtgatc gtcgccgtgc tgctcctgac ggctgtcaa      60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gttccctgag gtcgaccacc    120
aaagtctcca agtcgactag ctgcatgaaa gccgggtctt attgccgctc tactacgaga    180
acctgctgcg gttattgccc ttatttcggc aaattttgta ttgactttcc cagcaactga    240
tcttccccct actgtgctct atccttttct gcctctgcct gagtcctcct tacctgagag    300
tggtcatgaa ccactcatca cctgctcccc tggaggcctc agaggagcta caatgaaata    360
aaagccgcat tgcaaaaaaa aaaaaaaaaa aaa                                393
```

<210> 121

<211> 77

<212> PRT

<213> Conus consors

<400> 121

Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg Thr Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe Pro Ser Asn
65 70 75

<210> 122

<211> 35

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21 and 24 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 122

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Arg Ser Thr Thr Arg
1 5 10 15

Thr Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Phe Cys Ile Asp Phe
20 25 30

Xaa Ser Asn
35

<210> 123

<211> 361

<212> DNA

<213> Conus dalli

<400> 123

accaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg 60
acggcctgtc aactcatcac agctgatgac tccagaagta cgcagaagca tcgtgctctg 120
aggtcgacca tcaaacactc catgttgact aggagctgca cgctcccgg aggaccttgt 180
ggttattata atgactgctg cagtcatcaa tgcaatataa gcagaaataa atgcgagtag 240
ctgatccggc atctgatctt cccttctgt gctcgctcta acctgagagt ggatcatgaac 300
catcatcacc tactcctctg gaggcttcag aggagctaca tggaaataaa agccgcattg 360
c 361

<210> 124

<211> 73

<212> PRT

<213> Conus dalli

<400> 124

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Ile Lys His Ser Met Leu Thr Arg Ser Cys Thr
35 40 45

Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
50 55 60

Cys Asn Ile Ser Arg Asn Lys Cys Glu
65 70

<210> 125

<211> 28

<212> PRT

<213> Conus dalli

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4,

5 and 8 is Pro or Hyp; Xaa at residue 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 125

Ser Cys Thr Xaa Xaa Gly Gly Xaa Cys Gly Xaa Xaa Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Xaa
20 25

<210> 126

<211> 350

<212> DNA

<213> Conus distans

<400> 126

accaaaacca tcatacaaat gaaactgacg tgcgtgttga tcatcgccgt gctgttcctg 60
acggcctgtc aactcactag aggaaagctg gagcgtcctg ttctgaggtc gagcgaccaa 120
acctccgggt caacgaagag atgcgaagat cctggtgaac cttgcggaag tgatcattcc 180
tgctgcggcg gtagttgcaa ccacaacgtc tgcgcctgaa gctgggtctgg catctgacca 240
ttccccttct gtactctatc tctattgcct gagtcatctt tacctgtgag tggatcatgaa 300
tctctcaata ccttctcccc tggaggcttc agaagaacta gattgaaata 350

<210> 127

<211> 66

<212> PRT

<213> Conus distans

<400> 127

Met Lys Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Thr Arg Gly Lys Leu Glu Arg Pro Val Leu Arg Ser Ser
20 25 30

Asp Gln Thr Ser Gly Ser Thr Lys Arg Cys Glu Asp Pro Gly Glu Pro
35 40 45

Cys Gly Ser Asp His Ser Cys Cys Gly Gly Ser Cys Asn His Asn Val
50 55 60

Cys Ala
65

<210> 128

<211> 25

<212> PRT

<213> Conus distans

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 2 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 7 is Pro or Hyp

<400> 128

Cys Xaa Asp Xaa Gly Xaa Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
20 25

<210> 129
<211> 309
<212> DNA
<213> Conus ermineus

<400> 129
atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60
acagctgacg actccagacg tacgcagaag catcgtgccc tgaggctgac caccaaacgc 120
gccacgtcga atcgcccctg caagccgaaa ggacgaaaat gttttccgca tcagaaggac 180
tgctgcaata aaacgtgcac cagatcaaaa tgtccctgat cttccccctt ctgtgctgta 240
tccttttctg cctgagtcct ccttacctga gagtggtcag taaccactca tcaccatctc 300
ctctggagg 309

<210> 130
<211> 72
<212> PRT
<213> Conus ermineus

<400> 130
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
35 40 45
Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Asn Lys
50 55 60
Thr Cys Thr Arg Ser Lys Cys Pro
65 70

<210> 131
<211> 27
<212> PRT
<213> Conus ermineus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 1, 4, 11 and 27 is Pro or Hyp

<400> 131
Xaa Xaa Lys Xaa Lys Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1 5 10 15
Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Xaa
20 25

<210> 132
<211> 308
<212> DNA
<213> Conus ermineus

<400> 132
aactcatcac agctgatgac tccagaggta cgcagaacga tcgtgccctg aggtcgacca 60
ccaaactctc catgctgact cgggcctgct ggtcttccgg aacaccttgt ggtactgata 120
gtttatgctg cgggtggatgc aatgtatcca aaagtaaagt taactagctg attcggcgtc 180
tgaacttccc ccttctgtgc tctatccttt tctgcccagag tcctccatac ctgagaatgg 240
tcatgaacca ctcatcacct actcctctgg agacctcaga agagctacac tgaaataaaa 300
gcgcttgc 308

<210> 133
<211> 54
<212> PRT
<213> Conus ermineus

<400> 133
Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Asn Asp Arg Ala Leu
1 5 10 15
Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Ala Cys Trp Ser Ser
20 25 30
Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys Gly Gly Cys Asn Val
35 40 45
Ser Lys Ser Lys Cys Asn
50

<210> 134
<211> 27
<212> PRT
<213> Conus ermineus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at 8 residue is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
Trp

<400> 134
Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
1 5 10 15
Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
20 25

<210> 135
<211> 385
<212> DNA
<213> Conus geographus

<400> 135
ggatccatga aactgacgtg cgtgggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctggg gtcgaccacc 120
gaactctcct tgtcgactcg ctgcaagtca cccggatctt catgttcacc gactagttat 180
aattgctgca ggtcttgcaa tccatacgcc aaaagatggt acggctaata cagcgcctga 240
tcttccccct tctgtgctct atcccttctt gtctgagtcc tccttacctg agagtgggtca 300

tgaaccactc ctcacctact tctctggagg cttcggagga gctacattga aataaaagcc 360
gcattgtaaa aaaaaaaaaa aaaaa 385

<210> 136
<211> 73
<212> PRT
<213> Conus geographus

<400> 136
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
35 40 45
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
50 55 60
Asn Pro Tyr Ala Lys Arg Cys Tyr Gly
65 70

<210> 137
<211> 27
<212> PRT
<213> Conus geographus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Tyr

<400> 137
Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
1 5 10 15
Arg Ser Cys Asn Xaa Xaa Ala Lys Arg Cys Xaa
20 25

<210> 138
<211> 396
<212> DNA
<213> Conus geographus

<400> 138
ggatccatga aactgacgtg tgtggtgatc gtcgccgtgc tgctcctgac ggctgtcaa 60
ctcatcacag ctgatgactc cagaggtacg cagaagcatc gtgccctgag gtcgtccacc 120
aaactcacct tgtcgactcg ctgcaaatca cccggaactc catgttcaag gggtatgcgt 180
gattgctgca cgccttgctt gttatacagc aacaaatgta ggcgctacta acccagcgcc 240
tgatcttccc ccttctgtgc tctattcctt tctgcctgag tcctccttac ctgaaagtgg 300
tcatgaacca ctcatcacct acttctctgg aggcttcaga agagctacat tgaaataaaa 360
gccgcattgc aatgacaaaa aaaaaaaaaa aaaaaa 396

<210> 139
 <211> 74
 <212> PRT
 <213> Conus geographus

<400> 139
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 35 40 45
 Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Pro Cys
 50 55 60
 Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
 65 70

<210> 140
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 4, 7 and 18 is Pro or Hyp; Xaa at residue 22 and 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 140
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15
 Thr Xaa Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
 20 25

<210> 141
 <211> 407
 <212> DNA
 <213> Conus geographus

<400> 141
 ggaattccgt ttctgcgctg cttcctttgg catcaccaaa accatcatca aatgaaact 60
 gacgtgtgtg gtgatcgctg ccgtgctgct cctgacggcc tgtcaactca tcacagctga 120
 tgactccaga ggtacgcaga agcatcgctgc cctggggctg accaccgaac tctccttgctc 180
 gactcgctgc aagtcacccg gatcttcatg ttcaccgact agttataatt gctgcaggctc 240
 ttgcaatcca tacaccaaaa gatgttacgg ctaatccagc gcctgatctt ccctgctctg 300
 agtcctcctt acctgagagt ggtcatgaac cactcatcac ctacttctct aggcggttcg 360
 gaggagctac attgaaataa aagccgcatt gcaaaaaaaaa aaaaaaa 407

<210> 142
 <211> 73
 <212> PRT
 <213> Conus geographus

<400> 142
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Gly Ser Thr Thr Glu Leu Ser Leu Ser Thr Arg Cys Lys Ser
 35 40 45
 Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
 50 55 60
 Asn Pro Tyr Thr Lys Arg Cys Tyr Gly
 65 70

<210> 143
 <211> 27
 <212> PRT
 <213> Conus geographus
 <220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 143
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15
 Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa
 20 25

<210> 144
 <211> 28
 <212> PRT
 <213> Conus geographus
 <220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13, 22
 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
 or O-phospho-Tyr

<400> 144
 Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15
 Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys Xaa Gly
 20 25

<210> 145
 <211> 26
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and
 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or

O-phospho-Tyr

<400> 145

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Arg Ser Cys Asn Xaa Xaa Thr Lys Arg Cys
 20 25

<210> 146

<211> 314

<212> DNA

<213> Conus geographus

<400> 146

catcacagct gatgactcca gaggtacgca gaagcatcgt gccctgaggt cgtccaccāā 60
 actcaccttg tcgactcgct gcaaatacacc cggaactcca tgttcaaggg gtatgcgtga 120
 ttgctgcacg tcttgcttgt tatacagcaa caaatgtagg cgctactaac ccagcgctg 180
 atcttcccc ttctgtgctc tattcctttc tgcttgagtc ctcttacct gaaagtggtc 240
 atgaaccact catcacctac ttctctggag gcttcagaag agctacattg aaataaaagc 300
 cgcattgcaa tgac 314

<210> 147

<211> 55

<212> PRT

<213> Conus geographus

<400> 147

Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg Ala Leu Arg
 1 5 10 15

Ser Ser Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser Pro Gly Thr
 20 25 30

Pro Cys Ser Arg Gly Met Arg Asp Cys Cys Thr Ser Cys Leu Leu Tyr
 35 40 45

Ser Asn Lys Cys Arg Arg Tyr
 50 55

<210> 148

<211> 29

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
 spho-Tyr

<400> 148

Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15

Thr Ser Cys Leu Leu Xaa Ser Asn Lys Cys Arg Arg Xaa
 20 25

<210> 149
 <211> 29
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(29)
 <223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
 spho-Tyr

<400> 149
 Cys Lys Ser Xaa Gly Thr Xaa Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15
 Thr Ser Cys Leu Ser Xaa Ser Asn Lys Cys Arg Arg Xaa
 20 25

<210> 150
 <211> 380
 <212> DNA
 <213> Conus laterculatus

<400> 150
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac cgctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaatctctc catgctgact cggaagtgtt ggccttccgg aagctattgt 180
 cgtgcgaata gtaaattgctg cagtggatgc gatcggaaca gaaataaatg ttactagctg 240
 attcggcgctc tgaacttcct ccttctgtgc tctatccttt tctgcccagag tcctccatac 300
 ctgagagtgg tcatgaacca ctcaactcct actcctctgg aggcctcaga agagctacat 360
 tgaaataaaa gccgcattgc 380

<210> 151
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 151
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45
 Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
 50 55 60
 Asp Arg Asn Arg Asn Lys Cys Tyr
 65 70

<210> 152
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 152
 Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15
 Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Xaa
 20 25

<210> 153
 <211> 367-
 <212> DNA
 <213> Conus laterculatus

<400> 153
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaaactctc catatcgact cgctgccttc ctcccggatc atattgtaag 180
 gcgacaacgg aagtctgctg ctcttcttgc cttcaattcg ctacagatatg ttccgggttga 240
 tcttccctct tctgtgctct atccttttct gcctgagtc tccatacctg agaatgggtca 300
 tgaaccactc aacatctact cctctggagg cctcagaaga gctatatattga aataaaagcc 360
 gcattgc 367

<210> 154
 <211> 73
 <212> PRT
 <213> Conus laterculatus

<400> 154
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Ile Ser Thr Arg Cys Leu Pro
 35 40 45
 Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys Ser Ser Cys
 50 55 60
 Leu Gln Phe Ala Gln Ile Cys Ser Gly
 65 70

<210> 155
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 13 is Glu or gamma-carboxy Glu; Xaa at residue 3 a

nd 4 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 155

Cys Leu Xaa Xaa Gly Ser Xaa Cys Lys Ala Thr Thr Xaa Val Cys Cys
1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
20 25

<210> 156

<211> 373

<212> DNA

<213> Conus laterculatus

<400> 156

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aggtcgacca ccaatctctc catgtcgact cgctgcaagt ctcccggatc atcatgtagc 180
gtgtctatgc gtaactgctg cacttcttgc aattcacgca ccaagaaatg tacgcgacgt 240
ggctgaactt ccccttctg tgctctatcc ttttctgccc gagtcctcca tacctgagag 300
tggtcatgaa ccactcaaca tctactcctc tggaggcctc agaagagcta tattgaaata 360
aaagccgcat tgc 373

<210> 157

<211> 75

<212> PRT

<213> Conus laterculatus

<400> 157

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
35 40 45

Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys Thr Ser Cys
50 55 60

Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg Gly
65 70 75

<210> 158

<211> 29

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(29)

<223> Xaa at residue 3 is Pro or Hyp

<400> 158

Cys Lys Ser Xaa Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
20 25

<210> 159
<211> 330
<212> DNA
<213> Conus laterculatus

<400> 159
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aggtcgacaa ccaaactctc catgctgact cggacctgct ggccttccgg aacagcttgt 180
ggatttgata gtaactgctg cagtggatgc aatgtatcca gaagtaaagt taactagctg 240
attcggcgctc taaacttcct cttctgcct gagtcctcca tacctgagag tggatcatgaa 300
ccacatcatc acctcatctc tggaggcctc 330

<210> 160
<211> 72
<212> PRT
<213> Conus laterculatus

<400> 160
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Thr Cys Trp
35 40 45
Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys Ser Gly Cys
50 55 60
Asn Val Ser Arg Ser Lys Cys Asn
65 70

<210> 161
<211> 27
<212> PRT
<213> Conus laterculatus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
Trp

<400> 161
Thr Cys Xaa Xaa Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
1 5 10 15
Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
20 25

<210> 162
<211> 363
<212> DNA
<213> Conus laterculatus

<400> 162
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccttg 120
 aggtcgacca ccaatctctc catgctgact cggaagtgtt ggccttccgg aagctattgt 180
 cgtgcgaata gtaaagtctg cagtggatgc gatcggaaca gaagtaaagt taactagctg 240
 attcggcgtc taaacttcct ccttctgcct gagtcctcca tacctgagag tggatcatgaa 300
 ccactcatca cctactcctc tggaggcctc aaaggagcta cattgaaata aaagccgcat 360
 tgc 363

<210> 163
 <211> 72
 <212> PRT
 <213> Conus laterculatus

<400> 163
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
 35 40 45
 Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys Ser Gly Cys
 50 55 60
 Asp Arg Asn Arg Ser Lys Cys Asn
 65 70

<210> 164
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue4 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
 Trp; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr

<400> 164
 Lys Cys Xaa Xaa Ser Gly Ser Xaa Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15
 Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 165
 <211> 391
 <212> DNA
 <213> Conus leopardus

<220>
 <221> misc_feature
 <222> (1)..(391)
 <223> n may be any nucleotide

<400> 165
 atgaaactga cgtgtgtggt gatcgtagct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaag cgtcgtgctc tgaggctcgac caccaaactc 120
 tccaggctgc tctttgagtg cgcgccttcc ggtggacggt gtgggtttttt aaagtcctgc 180
 tgcgaaggat attgcatgg ggaaagcact tcatgtgtga gtggcccata cagcatctga 240
 tcttcccgcc ttcagtgtc tctcttttc tgctgagtc ctccatacct ctgagcggtc 300
 atgaaccact caacacctac tctctggag gcttcaggga actatattaa aataaagccg 360
 cattgcaacg aaanaaaaaa aaaaaaaaaa a 391

<210> 166
 <211> 79
 <212> PRT
 <213> Conus leopardus

<400> 166
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys Arg Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Leu Phe Glu Cys Ala
 35 40 45
 Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys Ser Cys Cys Glu Gly Tyr
 50 55 60
 Cys Asp Gly Glu Ser Thr Ser Cys Val Ser Gly Pro Tyr Ser Ile
 65 70 75

<210> 167
 <211> 37
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(37)
 <223> Xaa at residue 4, 20 and 26 is Glu or gamma-carboxy Glu; Xaa at r
 esidue 7 and 34 is Pro or Hyp; Xaa at residue 22 and 35 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 yr

<400> 167
 Ser Leu Phe Xaa Cys Ala Xaa Ser Gly Gly Arg Cys Gly Phe Leu Lys
 1 5 10 15
 Ser Cys Cys Xaa Gly Xaa Cys Asp Gly Xaa Ser Thr Ser Cys Val Ser
 20 25 30
 Gly Xaa Xaa Ser Ile
 35

<210> 168
 <211> 365
 <212> DNA
 <213> Conus leopardus

<400> 168
 atgaaactga cgtgtgtggt gatcgctcgct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgtggaag catcgtggtg tggggtcgac caccggactc 120
 tccccgtggc ccttggactg cacggctccc agtcaacctt gtggttatatt tcctaggtgc 180
 tgtggacatt gcgatgtacg cagggtatgt acgagtggct gatccggcgt ctgatctttc 240
 cgccttctgt gctgtatcct tttctgctg agtcctccat acccgtgagt ggcatgaac 300
 cactcaacac ctactcctct ggaggcttca gaggaactat attaaaataa agccgcattg 360
 caatg 365

<210> 169
 <211> 73
 <212> PRT
 <213> Conus leopardus

<400> 169
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Trp Lys His Arg
 20 25 30
 Gly Val Gly Ser Thr Thr Gly Leu Ser Pro Trp Pro Leu Asp Cys Thr
 35 40 45
 Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro Arg Cys Cys Gly His Cys
 50 55 60
 Asp Val Arg Arg Val Cys Thr Ser Gly
 65 70

<210> 170
 <211> 30
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 2, 8, 11 and 16 is Pro or Hyp; Xaa at residue 1 is
 Trp or Bromo Trp; Xaa at residue 14 is Tyr, 125I-Tyr, mono-iodo-
 Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 170
 Xaa Xaa Leu Asp Cys Thr Ala Xaa Ser Gln Xaa Cys Gly Xaa Phe Xaa
 1 5 10 15
 Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 171
 <211> 381
 <212> DNA
 <213> Conus leopardus

<400> 171
 atgaaactga cgtgtgtggt gatcgctcgct gtgctgttcc tgacggcctg tcaactcact 60
 acagctgaca tctccagagg tacgcggaag catcgtgctc tgaggtcgac caccaaactc 120

tccaggtcgc cctctaggtg catgtctccc ggtggaattt gtggtgattt tggtgactgc 180
 tgcgaaattt gcaatgtgta cggtatatgt gtgagtgact tacccggcac ctgatctttc 240
 cgcttctgt gctctatcct tttctgcctg agtcctccat acccctgagt ggtcatggac 300
 cactcaacac ctactcctct ggaggcttca gaggaactac attaaaataa agccgcattg 360
 caaaaaaaaa aaaaaaaaaa a 381

<210> 172
 <211> 77
 <212> PRT
 <213> Conus leopardus

<400> 172
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Ile Ser Arg Gly Thr Arg Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Ser Pro Ser Arg Cys Met
 35 40 45
 Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu Ile Cys
 50 55 60
 Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 65 70 75

<210> 173
 <211> 31
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 16 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 29 is Pro or Hyp; Xaa at residue 21 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 173
 Cys Met Ser Xaa Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Xaa
 1 5 10 15
 Ile Cys Asn Val Xaa Gly Ile Cys Val Ser Asp Leu Xaa Gly Ile
 20 25 30

<210> 174
 <211> 404
 <212> DNA
 <213> Conus leopardus

<400> 174
 atgaaactga cgtgtgtggt gatcgctcgt gtgctgttcc tgacggcctg tcaactcact 60
 acagctgatg attccagagg tacacggaag catcgtgctc tgaggtcaac caccaaactc 120
 tccaggtggc ccaggtactg cgcgcctccc ggtggagctt gtgggttttt tgatcactgc 180
 tgcggatatt gcgaaacgtt ttacaatacg tgtagatgag ttggctgatc cggcgcttga 240

tctttccgcc ttctgttgct ctatcttttt ctgcctgagt cctcccatac cccgttgagt 300
 ggtccatgaa ccactccaac acctactccc tccttggaag cttccaaagg aaacgacatt 360
 taaaataaat tccccattgc aattggaaaa aaaaaaaaaa aaaa 404

<210> 175
 <211> 72
 <212> PRT
 <213> Conus leopardus

<400> 175
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Arg Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Ser Arg Trp Pro Arg Tyr Cys Ala
 35 40 45
 Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys Gly Tyr Cys
 50 55 60
 Glu Thr Phe Tyr Asn Thr Cys Arg
 65 70

<210> 176
 <211> 27
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 20 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 5 is Pro or Hyp; Xaa at residue 1, 18 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176
 Xaa Cys Ala Xaa Xaa Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 5 10 15
 Gly Xaa Cys Xaa Thr Phe Xaa Asn Thr Cys Arg
 20 25

<210> 177
 <211> 292
 <212> DNA
 <213> Conus lynceus

<400> 177
 atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60
 acagctgatg actccagacg tacacagaag catcgtgccc tgaggctgac caccaatctc 120
 tccatgtcga ctgctgcaa gtctcccgga tcaccatgta gtgtgacatc gtataactgc 180
 tgcacttttt gctcttcata cactaagaaa tgtcgggcct ctttatgaac cactcatcac 240
 ctactcctct ggaggcctca gaagagctac actgaaataa aagccgcatt gg 292

<210> 178
 <211> 75

<212> PRT
 <213> Conus lynceus

<400> 178

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Ser
 35 40 45

Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys Thr Phe Cys
 50 55 60

Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
 65 70 75

<210> 179
 <211> 30
 <212> PRT
 <213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residue 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
 spho-Tyr

<400> 179

Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Val Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Thr Phe Cys Ser Ser Xaa Thr Lys Lys Cys Arg Ala Ser Leu
 20 25 30

<210> 180
 <211> 355
 <212> DNA
 <213> Conus lynceus

<400> 180

atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctcc tgacggcctg tcaactcatc 60

acagctgatg actccagagg tacgcagaag catcgtgccc tgaggctcgac caccaaacta 120

tccatgtata ctgctgctgc aggtccagga gcaatttgct ctaatagggt atgctgctgt 180

tattgcagta aaagaacaca tctatgtcat tcgcgaactg gctgatcttc ccccttctgt 240

gctctatcct ttttctgcct gagtcctcca tacctgagaa tggatcatgaa ccactcatca 300

cctactcctc ttggagacct cagaggagct aactgaaat aaaagccgca ttggc 355

<210> 181
 <211> 74
 <212> PRT
 <213> Conus lynceus

<400> 181

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Tyr Thr Arg Cys Ala Gly
35 40 45

Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr Cys Ser Lys
50 55 60

Arg Thr His Leu Cys His Ser Arg Thr Gly
65 70

<210> 182

<211> 28

<212> PRT

<213> Conus lynceus

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 16 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
r

<400> 182

Cys Ala Gly Xaa Gly Ala Ile Cys Xaa Asn Arg Val Cys Cys Gly Xaa
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
20 25

<210> 183

<211> 361

<212> DNA

<213> Conus lynceus

<400> 183

atgaaactga cgtgtgtggt gatcgtcgcc gtgctgctgc tagcggcctg tcaactacta 60

cacgctgatg actccagagg tacgcagaag actgctgccc gaggtcgacc accaaaactc 120

tccatgctga ctcgggcctg ctggtcttcc ggaacacctt gtggtactga tagtttatgc 180

tgcggtggat gcaatgtatc caaaagtaaa tgtaactagc tgattcggcg tctgaacttc 240

ccccttctgt gctctatcct tttctgccc agtcctccat acctgagaat ggtcatgaac 300

cactcatcac ctactcctct ggagacctca gaagagctac actgaaataa aagcgcattg 360

c 361

<210> 184

<211> 72

<212> PRT

<213> Conus lynceus

<400> 184

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Ala Ala
1 5 10 15

Cys Gln Leu Leu His Ala Asp Asp Ser Arg Gly Thr Gln Lys Thr Ala
20 25 30

Ala Arg Gly Arg Pro Pro Lys Leu Ser Met Leu Thr Arg Ala Cys Trp

		35				40					45				
Ser	Ser	Gly	Thr	Pro	Cys	Gly	Thr	Asp	Ser	Leu	Cys	Cys	Gly	Gly	Cys
	50					55					60				

Asn Val Ser Lys Ser Lys Cys Asn
65 70

<210>	185
<211>	27
<212>	PRT
<213>	Conus lynceus

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<220>
<221>  PEPTIDE
<222>  (I)..(27)
<223>  Xaa at residue 8 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
      Trp
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```
<400> 185
Ala Cys Xaa Ser Ser Gly Thr Xaa Cys Gly Thr Asp Ser Leu Cys Cys
1          5          10          15
```

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
20 25

<210>	186
<211>	364
<212>	DNA
<213>	Conus lynceus

```
<400> 186
atgaaactga cgtgtgtggt gatcgtcgcc gagctactcc taacggcctg tcaactcatc 60
acagctgatg actccagagg tacgcagaag catcgtgccc tgaggtcgac caccaatctc 120
tccatgctga ctcggaagtg ctggtctccc ggaacctatt gtcgtgcgca tagtaaattgc 180
tgccgtggat gcgatcagaa cagaaataaa tgttactagc tgattcggcg tctgaacttc 240
ctccttctgt gctctatcct ttttctgcct gagtcctcca tacctgagaa tggtcatgaa 300
ccactcatca cctactcctc tggaggcctc agaggagcct aactgaaat aaaagccgca 360
ttgg 364
```

```
<210> 187
<211> 72
<212> PRT
<213> Conus lynceus
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```
<400> 187
Met Lys Leu Thr Cys Val Val Ile Val Ala Glu Leu Leu Leu Thr Ala
1          5          10          15
```

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Asn Leu Ser Met Leu Thr Arg Lys Cys Trp
35 40 45

Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys Arg Gly Cys
50 55 60

Asp Gln Asn Arg Asn Lys Cys Tyr
65 70

<210> 188
<211> 27
<212> PRT
<213> Conus lynceus

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 5 is Pro or Hyp; Xaa at residue 3 is Trp or Bromo
Trp; Xaa at residue 8 and 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 188
Lys Cys Xaa Ser Xaa Gly Thr Xaa Cys Arg Ala His Ser Lys Cys Cys
1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Xaa
20 25

<210> 189
<211> 318
<212> DNA
<213> Conus magus

<400> 189
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aggtcggaca ccaaactctc catgtcgact cgctgcaagg gtacaggaaa accatgcagt 180
aggattgcgt ataactgctg caccggttct tgcagatcag gtaaagtgtg ctgatccagt 240
gcctgatctt ccccttctg tgctctatcc tttttctgcc tgagtctctc ttacctgaga 300
gtgggtcatga accactca 318

<210> 190
<211> 71
<212> PRT
<213> Conus magus

<400> 190
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45
Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
50 55 60
Cys Arg Ser Gly Lys Cys Gly
65 70

<210> 191
<211> 25
<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 191

Cys Lys Gly Thr Gly Lys Xaa Cys Ser Arg Ile Ala Xaa Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 192

<211> 259

<212> DNA

<213> Conus magus

<400> 192

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aagtcggaca ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180
ggtatttaca acgactgctg caatacatgc gatccagcca gaaagacatg tacgtagctg 240
atccggcgctc tgatcttcc 259

<210> 193

<211> 72

<212> PRT

<213> Conus magus

<400> 193

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Lys Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Thr Cys
50 55 60

Asp Pro Ala Arg Lys Thr Cys Thr
65 70

<210> 194

<211> 26

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 194
 Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Xaa Ala Arg Lys Thr Cys Thr
 20 25

<210> 195
 <211> 254
 <212> DNA
 <213> Conus magus

<400> 195
 gaatttttcag catcaccaaa accatcatca aaatgaaact gacgtgtgtg gtgatcgtcg 60
 ccgtgctgct cctgacggcc tgtcaactca tcacagctga tgactccaga ggtacgcaga 120
 agcatcgctgc cctgaggctcg gacaccaaac tctccatgtc aactcgctgc aagggtaaag 180
 gagcatcatg tcataggact tcgtatgact gctgcaccgg ttcttgcaac agaggtaaatt 240
 ttggctgatc cgcc 254

<210> 196
 <211> 71
 <212> PRT
 <213> Conus magus

<400> 196
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
 50 55 60
 Cys Asn Arg Gly Lys Phe Gly
 65 70

<210> 197
 <211> 25
 <212> PRT
 <213> Conus magus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
 -sulpho-Tyr or O-phospho-Tyr

<400> 197
 Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Xaa Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 198
 <211> 358

<212> DNA

<213> Conus miles

<400> 198

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ggatccatga aactgacgtg cgtggtgatc atcgccatgc tgttcctgac agcctatcaa      60
ctcgctacag ctgcgagcta cgccaaaggt aaacagaagc atcgtgctct gaggccagct      120
gacaaacacc tcaggttgac caagcgttgc aatgatcgcg gtggagggtg cagtcaacat      180
cctcactgct gcggtggaac ttgcaataag cttattggcg tatgtctgta aagctggtct      240
gccgtctgat attccctttc tgtgcttcat cctcttttgc ctgagtcatc catacctgtg      300
aatggttaag agccactcaa tacctattcc tctgggggct tcagaggaac tactttac      358

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<210> 199

<211> 74

<212> PRT

<213> Conus miles

<400> 199

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Met Lys Leu Thr Cys Val Val Ile Ile Ala Met Leu Phe Leu Thr Ala
1          5          10          15
Tyr Gln Leu Ala Thr Ala Ala Ser Tyr Ala Lys Gly Lys Gln Lys His
          20          25          30
Arg Ala Leu Arg Pro Ala Asp Lys His Leu Arg Leu Thr Lys Arg Cys
          35          40          45
Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly Gly
          50          55          60
Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
65          70

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<210> 200

<211> 27

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 12 is Pro or Hyp

<400> 200

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Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Xaa His Cys Cys Gly
1          5          10          15
Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
          20          25

```

<210> 201

<211> 292

<212> DNA

<213> Conus monachus

<400> 201

```

accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg      60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg      120

```

aggtcggaca ccaaactctc catatcgact cgctgcaagt ctacaggaaa atcatgcagt 180
 aggattgcgt ataactgctg caccggttct tgcagatcag gtaaagtgtg ctgatccagc 240
 gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct ta 292

<210> 202
 <211> 71
 <212> PRT
 <213> Conus monachus

<400> 202
 Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15

~~Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg~~
 20 25 30

Ala Leu Arg Ser Asp Thr Lys Leu Ser Ile Ser Thr Arg Cys Lys Ser
 35 40 45

Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
 50 55 60

Cys Arg Ser Gly Lys Cys Gly
 65 70

<210> 203
 <211> 25
 <212> PRT
 <213> Conus monachus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 203
 Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 204
 <211> 258
 <212> DNA
 <213> Conus monachus

<400> 204
 accaaaacca tcatcaaaat gaaactgacg agtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaacctctc catgtcgact cgctgcaagg gtaaaggatc ttcatgtagt 180
 aggaccatgt ataactgctg caccggttct tgcaacagag gtaaagtgtg ctgatccagc 240
 gcctgatctt cccccttc 258

<210> 205
 <211> 71
 <212> PRT

<213> Conus monachus

<400> 205

Met Lys Leu Thr Ser Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Asp Thr Asn Leu Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys Thr Gly Ser
50 55 60

Cys Asn Arg Gly Lys Cys Gly
65 70

<210> 206

<211> 25

<212> PRT

<213> Conus monachus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 206

Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Xaa Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 207

<211> 258

<212> DNA

<213> Conus obscurus

<400> 207

ctctctctct ctctgctgga caggctgcct ccctgcatga aaggcggatc gtcatgccgc 60

ggtactacgg gagtctgttg cggtttttgc agtgatttcg gctataaatg tagggactat 120

ccccaaaact gatcttcccc cttctgtgct ctatcctttt ctgtccgagt cctcctgacc 180

tgagagtggg catgaaccac tcatcaccta ccctctggg gcttcacagg atctacattg 240

aaataaaagc cgcattgc 258

<210> 208

<211> 39

<212> PRT

<213> Conus obscurus

<400> 208

Leu Leu Asp Arg Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg
1 5 10 15

Gly Thr Thr Gly Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys
20 25 30

Cys Arg Asp Tyr Pro Gln Asn
35

<210> 209
<211> 35
<212> PRT
<213> Conus obscurus

<220>
<221> PEPTIDE
<222> (1)..(35)
<223> Xaa at residue 2, 3 and 33 is Pro or Hyp; Xaa at residue 27 and 32 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 209
Ser Xaa Xaa Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Xaa Lys Cys Arg Asp Xaa
20 25 30

Xaa Gln Asn
35

<210> 210
<211> 259
<212> DNA
<213> Conus obscurus

<400> 210
ctctctctct ctctgctgga caggctcgact cgctgcttgc ctgacggaac gtcttgcctt 60
tttagtagga tcagatgctg cggtacttgc agttcaatct taaagtcattg tgtgagctga 120
tccagcggtt gatcttcctc cctctgtgct ccattccttt ctgcctgagt tctccttacc 180
tgagagtggc catgaaccac tcatcaccta ctcttctgga ggcttcagag gagctacatt 240
gaaataaaaag ccgcattgc 259

<210> 211
<211> 32
<212> PRT
<213> Conus obscurus

<400> 211
Arg Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg
1 5 10 15

Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25 30

<210> 212
<211> 28
<212> PRT
<213> Conus monachus

<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 3 is Pro or Hyp

<400> 212

Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
 20 25

<210> 213
 <211> 330
 <212> DNA
 <213> Conus pulicarius

<220>
 <221> misc_feature
 <222> (1)..(330)
 <223> n may be any nucleotide

<400> 213
 atgaaactga cgtgtgtggt gatcatcgcc gtgctgttcc tgacggcctg tcaactcatt 60
 acagctgaga cttactccag aggtaagcag aagcacccgtg ctttgaggtc aactgacaaa 120
 aactccaagt tgactaggca gtgctcgcct aacggtggat cttgttctcg tcattttcac 180
 tgctgcagcc tctattgcaa taaaaatact ggcgtatgta ttgcaaccta ataccctgtg 240
 gtggtcatga accactcaat accctctcct ctggaggcct cagaggaact gcattgaaat 300
 aaaactgcat tgcnttgacc aaaaaaaaaa 330

<210> 214
 <211> 76
 <212> PRT
 <213> Conus pulicarius

<400> 214
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Lys His
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Gln Cys
 35 40 45

Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys Ser Leu
 50 55 60

Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
 65 70 75

<210> 215
 <211> 30
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(30)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 4 is Pro or H
 yp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Ty
 r, O-sulpho-Tyr or O-phospho-Tyr

<400> 215
 Xaa Cys Ser Xaa Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys

<210>	219
<211>	340
<212>	DNA
<213>	Conus purpurascens

<400> 219
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcgacca ccaaactctt cacgtcgaaa agctgcaagc ttcccggagc atattgtaat 180
 gcagaagatt atgactgctg ccttagatgc aaagttggag gtacatgtgg ctgatccagt 240
 gcctgatctt cccccttctg tgctctatcc ttttctgcct gagtcctcct tacctaagag 300
 tggatcatgaa ccactcatca ccttctcctc tggaggcttc 340

<210> 220
 <211> 71
 <212> PRT
 <213> Conus purpurascens

<400> 220
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Leu Phe Thr Ser Lys Ser Cys Lys Leu
 35 40 45
 Pro Gly Ala Tyr Cys Asn Ala Glu Asp Tyr Asp Cys Cys Leu Arg Cys
 50 55 60
 Lys Val Gly Gly Thr Cys Gly
 65 70

<210> 221
 <211> 26
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 12 is Glu or gamma-carboxy Glu; Xaa at residue 5 is Pro or Hyp; Xaa at residue 8 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 221
 Ser Cys Lys Leu Xaa Gly Ala Xaa Cys Asn Ala Xaa Asp Xaa Asp Cys
 1 5 10 15
 Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
 20 25

<210> 222
 <211> 317
 <212> DNA
 <213> Conus purpurascens

<400> 222
 atgaaactga cgtgtgtggt gatcgctgcc gtgctgttcc tgacggcctg tcaactcatc 60
 acagctgatg actccagacg tacgcagaag catcgtgccc tgaggtegac caccaaacgc 120
 gccacgtcga atcgcccctg caagaaaacc ggacgaaaat gttttccgca tcagaaggac 180

tgctgcggtc gagcgtgcat catcacaata tgtccctgat cttccccctt ctgtgctgta 240
 tccttttctg cctgagtcct ccttacctga gagtggtcat gaaccactca tcaccttctc 300
 ctctggaggc ttcagag 317

<210> 223
 <211> 72
 <212> PRT
 <213> Conus purpurascens

<400> 223
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Arg Thr Gln Lys His Arg
 20 25 30
 Ala Leu Arg Ser Thr Thr Lys Arg Ala Thr Ser Asn Arg Pro Cys Lys
 35 40 45
 Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys Cys Gly Arg
 50 55 60
 Ala Cys Ile Ile Thr Ile Cys Pro
 65 70

<210> 224
 <211> 27
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1, 11 and 27 is Pro or Hyp

<400> 224
 Xaa Cys Lys Lys Thr Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
 1 5 10 15
 Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Xaa
 20 25

<210> 225
 <211> 328
 <212> DNA
 <213> Conus radiatus

<400> 225
 gctgatgcct gatcttcacg gttcttcctt gtctcctttg gcatcaccaa aaccatcatc 60
 aaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 120
 atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggggc gatcagcagt 180
 ctctttaagt cgaccogtca tggctgcaaa cccctcaaac gtcgttggtt caatgataaa 240
 gaatgctgca gcaaattttg caattcagtc cgaaagcagt gtggataaat ggctaaaaaa 300
 ctgaataaaa gccgcattgc aaaaaaaa 328

<210> 226
 <211> 74

<212> PRT
 <213> Conus radiatus

<400> 226
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
 20 25 30
 Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg His Gly Cys
 35 40 45
 Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
 50 55 60
 Phe Cys Asn Ser Val Arg Lys Gln Cys Gly
 65 70

<210> 227
 <211> 28
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(28)
 <223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 i
 s Pro or Hyp

<400> 227
 His Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
 1 5 10 15
 Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
 20 25

<210> 228
 <211> 250
 <212> DNA
 <213> Conus radiatus

<400> 228
 gaaatgaaac tgacgtgtgt ggtgatcgtc gccgtgctgg tcctgacggc ctgtcaactc 60
 atcacagctg atgactccag aggtatgcag aaacatcatg ccctgggggc gatcagcagt 120
 ctctttaagt cgaccgctcg tggctgcaaa cccctcaaac gtcgttggtt caatgataaa 180
 gaatgctgca gcaaattttg caattcagtc cgaaaccagt gtggataaat ggctaaaaaac 240
 tgaataaaaag 250

<210> 229
 <211> 74
 <212> PRT
 <213> Conus radiatus

<400> 229
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
 20 25 30

Ala Leu Gly Ser Ile Ser Ser Leu Phe Lys Ser Thr Arg Arg Gly Cys
35 40 45

Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys Cys Ser Lys
50 55 60

Phe Cys Asn Ser Val Arg Asn Gln Cys Gly
65 70

<210>	230
<211>	28
<212>	PRT
<213>	Conus radiatus

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<220>
<221> PEPTIDE
<222> (1)..(28)
<223> Xaa at residue 15 is Glu or gamma-carboxy Glu; Xaa at residue 5 is
      s Pro or Hyp
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<400> 230
Arg Gly Cys Lys Xaa Leu Lys Arg Arg Cys Phe Asn Asp Lys Xaa Cys
1          5          10          15
```

Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
20 25

<210>	231
<211>	435
<212>	DNA
<213>	Conus radiatus

<400>	231					
ggaattccgc	ttgcacggcg	aacctgactt	catctttctt	ccctgcctcc	tttggcatca	60
ccaaaaccat	catcaaaatg	aaactgacgt	gtgtggtgat	cgtcgccgtg	ctggtcctga	120
cggcctgtca	actcatcaca	gctgatgact	ccagagggtat	gcagaagcat	catgccctga	180
ggtcgatcac	caaactctcc	ctgtcgactc	gctgcaaacc	tcccggatca	ccatgtagag	240
tttcttcgta	taactgctgc	tcttcttgca	aatcatacaa	caagaaatgt	ggctgaactt	300
ccccttctgt	gctctatcct	tttcctgccc	gagtcctcca	tacctgagag	tagtcatgaa	360
ccactgatta	cctactcctc	tggagggcct	cagaggagct	actttgaaat	aaaagcccgc	420
attgcaaaaa	aaaaa					435

<210>	232
<211>	72
<212>	PRT
<213>	Conus radiatus

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<400> 232
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Val Leu Thr Ala
1          5          10          15
```

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Met Gln Lys His His
20 25 30

Ala Leu Arg Ser Ile Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Pro
35 40 45

Pro Gly Ser Pro Cys Arg Val Ser Ser Tyr Asn Cys Cys Ser Ser Cys
 50 55 60

Lys Ser Tyr Asn Lys Lys Cys Gly
 65 70

<210> 233
 <211> 27
 <212> PRT
 <213> Conus radiatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 3, 4 and 7 is Pro or Hyp; Xaa at residue 13 and 22
 is Tyr, ¹²⁵I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
 phospho-Tyr

<400> 233
 Cys Lys Xaa Xaa Gly Ser Xaa Cys Arg Val Ser Ser Xaa Asn Cys Cys
 1 5 10 15

Ser Ser Cys Lys Ser Xaa Asn Lys Lys Cys Gly
 20 25

<210> 234
 <211> 392
 <212> DNA
 <213> Conus rattus

<400> 234
 ggatccatga aactgacgtg catggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
 ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120
 gacaaacaca tcagggttgac caagcggttg aatgctcgca atgatggttg cagtcaacat 180
 tctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctggtct 240
 gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg 300
 aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360
 aaagccacat tgcaaaaaaaaa aaaaaaaaaa aa 392

<210> 235
 <211> 74
 <212> PRT
 <213> Conus rattus

<400> 235
 Met Lys Leu Thr Cys Met Val Ile Ile Ala Val Leu Phe Leu Thr Ala
 1 5 10 15
 Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
 20 25 30
 Pro Thr Leu Arg Pro Ala Asp Lys His Ile Arg Leu Thr Lys Arg Cys
 35 40 45
 Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser Gly
 50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
65 70

<210> 236
<211> 27
<212> PRT
<213> Conus rattus

<400> 236
Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
20 25

<210> 237
<211> 395
<212> DNA
<213> Conus rattus

<400> 237
ggatccatga aactgacgtg cgtggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
ctcgatgcag ctgcgagcta cgacaaaggt aagcagaaac ctccctactct gaggccagct 120
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180
cctcaatgct gcagtggatc ttgcaataag actgcaggcg tatgtctgta aagctgggtct 240
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg 300
aatggttaag agccactcaa tacctactcc tctggggggt tcagaggaac tacattaaat 360
aaagccacat tgcaacgaaa aaaaaaaaaa aaaaa 395

<210> 238
<211> 74
<212> PRT
<213> Conus rattus

<400> 238
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Asp Ala Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
50 55 60

Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
65 70

<210> 239
<211> 27
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(27)

<223> Xaa at residue 12 is Pro or Hyp

<400> 239

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
1 5 10 15

Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
20 25

<210> 240

<211> 390

<212> DNA

<213> Conus rattus

<400> 240

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ggatccatga aactgacgtg tgtgggtgatc atcgccgtgc tgttcctgac agcctgtcaa 60
ttcgatacag ctgcgagcta cgacaaaggt aagcagaaac ctctactct gaggccagct 120
gacaaacact tcaggttgat caagcgttgc aatgctcgca atagtggttg cagtcaacat 180
cctcaatgct gcagtggatc ttgcaataag actttgggcg tatgtctgta aagctggctct 240
gccgtctgat attccctttc tgtgctttat cctcttttgc ctgagtcatc catacctgtg 300
aatggttaag agccactcaa tacctactcc tctgggggct tcagaggaac tacattaaat 360
aaagccacat tgaaaaaaaa aaaaaaaaaa 390

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<210> 241

<211> 74

<212> PRT

<213> Conus rattus

<400> 241

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Phe Asp Thr Ala Ala Ser Tyr Asp Lys Gly Lys Gln Lys Pro
20 25 30

Pro Thr Leu Arg Pro Ala Asp Lys His Phe Arg Leu Ile Lys Arg Cys
35 40 45

Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser Gly
50 55 60

Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
65 70

<210> 242

<211> 27

<212> PRT

<213> Conus rattus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 12 is Pro or Hyp

<400> 242

Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Xaa Gln Cys Cys Ser
1 5 10 15

Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
20 25

<210> 243
<211> 379
<212> DNA
<213> Conus stercusmuscarum

<400> 243
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
aggtcgaaga ccaaactctc catgtcgact cgctgcaaga gtaaaggagc aaaatgttca 180
aggcttatgt atgactgctg cagcgggttct tgcagcggct acacaggtag atgtggctga 240
tccagcgcct gatcttcccc cttctgtgct ctatcctttt ctgcctgggt cctccttacc 300
tgagagtggc catgaaccac tcatcaccta ctctcttgga ggcctcagag gagttacaat 360
gaaataaaaag ccgcattgc 379

<210> 244
<211> 73
<212> PRT
<213> Conus stercusmuscarum

<400> 244
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ser
35 40 45
Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys Ser Gly Ser
50 55 60
Cys Ser Gly Tyr Thr Gly Arg Cys Gly
65 70

<210> 245
<211> 27
<212> PRT
<213> Conus stercusmuscarum

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 13 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 245
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Xaa Asp Cys Cys
1 5 10 15
Ser Gly Ser Cys Ser Gly Xaa Thr Gly Arg Cys
20 25

<210> 246
<211> 35

<212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(35)
 <223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
 -phospho-Tyr

<400> 246
 Thr Thr Ser Cys Met Gln Ala Gly Ser Xaa Cys Gly Ser Thr Thr Arg
 1 5 10 15
 Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Lys Cys Ile Asp Xaa
 20 25 30

Xaa Ser Asn
 35

<210> 247
 <211> 380
 <212> DNA
 <213> Conus stercusmuscarum

<400> 247
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acgacctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccttg 120
 aggtcgaaga ccaaactctc catgttaact ttgcgctgcg catcttacgg aaaaccttgt 180
 ggtattgaca acgactgctg caatgcatgc gatccagcca gaaatatatg tacgtagctg 240
 atccggcgtc tgatcttccc ccttctgtgc tctatccttt tctgcctgag tcctccttac 300
 ctgagagtgg tcatgaacca ctcatcatct actctcctgg aggcctcaga ggagctacaa 360
 tgaaataaaa gccgcattgc 380

<210> 248
 <211> 72
 <212> PRT
 <213> Conus stercusmuscarum

<400> 248
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Thr
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Ala
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
 50 55 60
 Asp Pro Ala Arg Asn Ile Cys Thr
 65 70

<210> 249
 <211> 26
 <212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
r

<400> 249

Cys Ala Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
20 25

<210> 250

<211> 388

<212> DNA

<213> Conus stercusmuscarum

<400> 250

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ggatccatga aactgacgtg tgtggtgatt gtcgccgtgc tgctcctgac ggccctgtcaa      60
ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcgaagacc      120
aaactctcca tgttaacttt gcgctgcgta tcttacggaa aaccttgtgg tattgacaac      180
gactgctgca atgcatgcga tccagccaga aatatatgta cgtagctgat ccggcgtctg      240
atcttcccccc ttctgtgctc tatccttttc tgccctgggtc ctcccttacct gagagtggtc      300
atgaaccact catcacctac tcctctggag gcctcagagg agttacaatg aaataaaagc      360
cgcatgtgcaa aaaaaaaaaa aaaaaaaaaa      388

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<210> 251

<211> 72

<212> PRT

<213> Conus stercusmuscarum

<400> 251

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
20 25 30

Ala Leu Arg Ser Lys Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Val
35 40 45

Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn Ala Cys
50 55 60

Asp Pro Ala Arg Asn Ile Cys Thr
65 70

<210> 252

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 7 and 20 is Pro or Hyp; Xaa at residue 4 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty
r

<400> 252

Cys Val Ser Xaa Gly Lys Xaa Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Xaa Ala Arg Asn Ile Cys Thr
20 25

<210> 253

<211> 264

<212> DNA

<213> Conus striatus

<400> 253

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60

acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgttccttg 120

aggtcgacca ccaaagtctc caaggcgact gactgcattg aagccggaaa ttattgcgga 180

cctactgtta tgaaaatctg ctgcggcttt tgcagtccat acagcaaaat atgtatgaac 240

tatcccaaaa attgatcttc cccc 264

<210> 254

<211> 78

<212> PRT

<213> Conus striatus

<400> 254

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ala Thr Asp Cys Ile Glu
35 40 45

Ala Gly Asn Tyr Cys Gly Pro Thr Val Met Lys Ile Cys Cys Gly Phe
50 55 60

Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn Tyr Pro Lys Asn
65 70 75

<210> 255

<211> 36

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
25 and 34 is Pro or Hyp; Xaa at residue 10, 26 and 33 is Tyr, 125
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 255

Ala Thr Asp Cys Ile Xaa Ala Gly Asn Xaa Cys Gly Xaa Thr Val Met
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Xaa Xaa Ser Lys Ile Cys Met Asn
 20 25 30

Xaa Xaa Lys Asn
 35

<210> 256
 <211> 233
 <212> DNA
 <213> Conus striatus

<400> 256
 gtcgactcgc tgcaagctta aaggacaatc atgtcgtagg actatgtatg actgctgcag 60
 cggttcttgc ggcaggagag gtaaatgtgg ctgatccagc gcctgatctc ccccttctg 120
 tgctctatcc ttttctgcct gggtcctcct tacctgagag tggatcatgaa ccactcatca 180
 cctactcctc tggaggcctc agaggagcta caatgaaata aaagccgcat tgc 233

<210> 257
 <211> 30
 <212> PRT
 <213> Conus striatus

<400> 257
 Ser Thr Arg Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr
 1 5 10 15

Asp Cys Cys Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys Gly
 20 25 30

<210> 258
 <211> 26
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
 -sulpho-Tyr or O-phospho-Tyr

<400> 258
 Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Xaa Asp Cys Cys
 1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
 20 25

<210> 259
 <211> 310
 <212> DNA
 <213> Conus striatus

<400> 259
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc aactcatcac agctgatgac tccagaggta cgcagaagca tcgtgccctg 120
 aggtcggaca ccaaactctc catgtcgact cgctgcaagg ctgcaggaaa atcatgcagt 180
 aggattgcgt ataactgctg caccgggttct tgcagatcag gtaaatgcgg ctgatccagc 240

gcctgatctt ccccttctg tgctctatcc tttctgcctg agtcctctta cctgagagtg 300
gtcatgaacc 310

<210> 260
<211> 71
<212> PRT
<213> Conus striatus

<400> 260
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Ser Thr Arg Cys Lys Ala
35 40 45
Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys Thr Gly Ser
50 55 60
Cys Arg Ser Gly Lys Cys Gly
65 70

<210> 261
<211> 25
<212> PRT
<213> Conus striatus

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
-sulpho-Tyr or O-phospho-Tyr

<400> 261
Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Xaa Asn Cys Cys
1 5 10 15
Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 262
<211> 256
<212> DNA
<213> Conus striatus

<400> 262
acaaaacca tcatcaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc aactcatcac agctgatgac tccagaggta cgcaggagca tcgtgccctg 120
aggtcggaca ccaaactctc catgttaact ttgcgctgcg aatcttacgg aaaaccttgt 180
ggtatttaca acgactgctg caatgcatgc gatccagcca aaaagacatg tacgtagctg 240
atccggcgctc tgatct 256

<210> 263
<211> 72
<212> PRT
<213> Conus striatus

<400> 263
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Ser Met Leu Thr Leu Arg Cys Glu
 35 40 45
 Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn Ala Cys
 50 55 60
 Asp Pro Ala Lys Lys Thr Cys Thr
 65 70

<210> 264
 <211> 26
 <212> PRT
 <213> Conus striatus

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 2 is Glu or gamma-carboxy Glu; Xaa at residue 7 and
 20 is Pro or Hyp; Xaa at residue 4 and 11 is Tyr, 125I-Tyr, mon
 o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 264
 Cys Xaa Ser Xaa Gly Lys Xaa Cys Gly Ile Xaa Asn Asp Cys Cys Asn
 1 5 10 15
 Ala Cys Asp Xaa Ala Lys Lys Thr Cys Thr
 20 25

<210> 265
 <211> 229
 <212> DNA
 <213> Conus striatus

<400> 265
 tctaggtcct ccggcagccc ctgtggtggt actagtatat gctgtggttag atgctatagg 60
 ggtaaatgta cgtagctcat cgggcgtctg atcttcccc ttctgtgctc catccttttc 120
 tgccctgagtc ctcttacct gagagtgggc gtgaaccact catcgccctac tcctctggag 180
 gcttcagagg ggctacacta aaataaaagc tatattgcaa tgaaaaaaa 229

<210> 266
 <211> 24
 <212> PRT
 <213> Conus striatus

<400> 266
 Cys Arg Ser Ser Gly Ser Pro Cys Gly Val Thr Ser Ile Cys Cys Gly
 1 5 10 15
 Arg Cys Tyr Arg Gly Lys Cys Thr
 20

<210> 267
 <211> 24
 <212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 19 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 267

Cys Arg Ser Ser Gly Ser Xaa Cys Gly Val Thr Ser Ile Cys Cys Gly
1 5 10 15

Arg Cys Xaa Arg Gly Lys Cys Thr
20

<210> 268

<211> 26

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 268

Cys Lys Leu Lys Gly Gln Ser Cys Arg Lys Thr Ser Xaa Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Gly Arg Ser Gly Lys Cys
20 25

<210> 269

<211> 292

<212> DNA

<213> Conus striolatus

<400> 269

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgtctt gctgctcctg 60
acgacctgtc gtctcatcac agctgatgac tccagaggta cgcagaagca tcgttccttg 120
aggtcgacta ctaaagtctc catgtcgact cgctgcaagg gtaaaggagc atcatgtctt 180
aggactgcgt atgactgctg caccggttct tgcaacagag gtagatgtgg ctgatccagc 240
gtctgatctt ccccttctg tgctctatcc ttttctgctt gagtcctcct ta 292

<210> 270

<211> 71

<212> PRT

<213> Conus striolatus

<400> 270

Met Lys Leu Thr Cys Val Val Ile Val Val Leu Leu Leu Leu Thr Thr
1 5 10 15

Cys Arg Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Met Ser Thr Arg Cys Lys Gly
35 40 45

Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys Thr Gly Ser
 50 55 60

Cys Asn Arg Gly Arg Cys Gly
 65 70

<210> 271
 <211> 25
 <212> PRT
 <213> Conus striolatus

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
 -----sulpho-Tyr-or-O-phospho-Tyr-----

<400> 271
 Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Xaa Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 272
 <211> 259
 <212> DNA
 <213> Conus striolatus

<400> 272
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgctgacg 60
 gcgtgtcaac tcatacacagc tgaggactcc agaggtacac agaagcatcg taccctgagg 120
 tcgaccgtca gacgctccaa gtccgagttg actacgagat gcaggccttc aggatccaac 180
 tgtggtaata ttagtatctg ctgtggtaga tgcgttaaca gaagatgtac gtagctcatc 240
 gggcgtctga tctttcccc 259

<210> 273
 <211> 71
 <212> PRT
 <213> Conus striolatus

<400> 273
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Thr Ala Cys
 1 5 10 15

Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg Thr
 20 25 30

Leu Arg Ser Thr Val Arg Arg Ser Lys Ser Glu Leu Thr Thr Arg Cys
 35 40 45

Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly Arg
 50 55 60

Cys Val Asn Arg Arg Cys Thr
 65 70

<210> 274
 <211> 24
 <212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 3 is Pro or Hyp

<400> 274

Cys Arg Xaa Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr
20

<210> 275

<211> 280

<212> DNA

<213> Conus striolatus

<400> 275

accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt tctgttcctg 60
acggcgtgtc aactcatcac agctgaggac tccagaggta cacagaagca tcgttcctg 120
aggctcgacta ccaaagtctc caagtcgact agctgcatga aagccgggtc ttattgcgtc 180
gctactacga gaatctgctg cggttattgc gcttatttcg gcaaaatatg tattgactat 240
cccaaaaact gatcttcccc ctactgtgct ctatcctttt 280

<210> 276

<211> 77

<212> PRT

<213> Conus striolatus

<400> 276

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Lys His Arg
20 25 30

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr Pro Lys Asn
65 70 75

<210> 277

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> PEPTIDE

<222> (1)..(35)

<223> Xaa at residue 33 is Pro or Hyp; Xaa at residue 10, 21, 24 and 32
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-
phospho-Tyr

<400> 277

Ser Thr Ser Cys Met Lys Ala Gly Ser Xaa Cys Val Ala Thr Thr Arg
 1 5 10 15

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Asp Xaa
 20 25 30

Xaa Lys Asn
 35

<210> 278

<211> 174

<212> DNA

<213> Conus textile

<400> 278

gttgactcgg tactgcacgc ctcatggagg acattgtggt tatcataatg actgctgcag 60

tcatcaatgc aatataaaca gaaataaatg tgagtagctg atctggcatc tgatctgtgc 120

tcgtccttac ctgagagtgg tcatgaacca ctcatcacct actcctctgg aggc 174

<210> 279

<211> 31

<212> PRT

<213> Conus textile

<400> 279

Leu Thr Arg Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn
 1 5 10 15

Asp Cys Cys Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25 30

<210> 280

<211> 28

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is
 s Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-
 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 280

Xaa Cys Thr Xaa His Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 281

<211> 28

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is
 s Pro or Hyp; Xaa at residue 1 and 11 is Tyr, 125I-Tyr, mono-iodo-
 -Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 281
 Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa His Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
 20 25

<210> 282
 <211> 379
 <212> DNA
 <213> Conus tulipa

<400> 282
 accaaaacca tcatacaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 --- -- - - - acggcctgtc-agctcatcac-agctctgcac-tccagaggta-cgcagaagca-tcgtgccctg 120
 gggcggacca ccaaactcac cttgtcgact cgctgcaaata cacccggtac tccatgttca 180
 ccgactagtt ataattgctg ctggtcttgc agtccataca gaaaaaatg taggggctaa 240
 tccagcgcct gattttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300
 tgaaagtggg catgaaccac tcataccta cttctctgga ggcttcggag gagctacatt 360
 gaaataaaaag ccgcattgc 379

<210> 283
 <211> 73
 <212> PRT
 <213> Conus tulipa

<400> 283
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
 20 25 30
 Ala Leu Gly Arg Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Lys Ser
 35 40 45
 Pro Gly Ser Pro Cys Ser Pro Thr Ser Tyr Asn Cys Cys Trp Ser Cys
 50 55 60
 Ser Pro Tyr Arg Lys Lys Cys Arg Gly
 65 70

<210> 284
 <211> 27
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 3, 7, 10 and 21 is Pro or Hyp; Xaa at residue 17 is
 Trp or Bromo Trp; Xaa at residue 13 and 22 is Tyr, 125I-Tyr, mo
 no-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 284
 Cys Lys Ser Xaa Gly Ser Xaa Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
 1 5 10 15

Xaa Ser Cys Ser Xaa Xaa Arg Lys Lys Cys Arg
20 25

<210> 285
<211> 379
<212> DNA
<213> Conus tulipa

<400> 285
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
acggcctgtc agctcatcac agctctgcac tccagaggta cgcagaagca tcgtgccctg 120
gggtcgacca ccaaactcac cttgtcgact cgctgcttgt caccggatc ttcattgttca 180
ccgactagtt ataattgctg caggtcttgc aatccatata gcagaaaatg taggggctaa 240
tccagcgctt gatcttcccc cttctgtgct ctattccttt ctgcctgagt cctccttacc 300
tgaaagtggc catgaaccac tcatcaccta cttctctgga ggcttcggag gagctacatt 360
gaaataaaag ccgcattgc 379

<210> 286
<211> 73
<212> PRT
<213> Conus tulipa

<400> 286
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15
Cys Gln Leu Ile Thr Ala Leu His Ser Arg Gly Thr Gln Lys His Arg
20 25 30
Ala Leu Gly Ser Thr Thr Lys Leu Thr Leu Ser Thr Arg Cys Leu Ser
35 40 45
Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys Arg Ser Cys
50 55 60
Asn Pro Tyr Ser Arg Lys Cys Arg Gly
65 70

<210> 287
<211> 27
<212> PRT
<213> Conus tulipa

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residue 4, 10 and 21 is Pro or Hyp; Xaa at residue 13 and
22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr

<400> 287
Cys Leu Ser Xaa Gly Ser Ser Cys Ser Xaa Thr Ser Xaa Asn Cys Cys
1 5 10 15
Arg Ser Cys Asn Xaa Xaa Ser Arg Lys Cys Arg
20 25

<210> 288

<211> 401
 <212> DNA
 <213> Conus viola

<400> 288
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgatgac tccagaggta cgcagttgca tcgtgccctg 120
 aggaaggcca ccaaactccc cgtgtcgact cgctgcatta ctttaggaac acgatgtaag 180
 gttccgagtc aatgctgcag atcttcttgc aagaacggtc gttgtgctcc atcccctgaa 240
 gaatggtaaa tgtggctgat ccagcgcttg atcttcccc ttctgactgt ctccgacctt 300
 ttctgactga gtccctcctta cctgagaggc gtcatgaacc actcatcacc tactcccctg 360
 gaagcttcag aggagctaca ttgaaataaa agccgcattg c 401

<210> 289
 <211> 76
 <212> PRT
 <213> Conus viola

<400> 289
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Leu His Arg
 20 25 30
 Ala Leu Arg Lys Ala Thr Lys Leu Pro Val Ser Thr Arg Cys Ile Thr
 35 40 45
 Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg Ser Ser Cys
 50 55 60
 Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
 65 70 75

<210> 290
 <211> 31
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(31)
 <223> Xaa at residue 29 and 30 is Glu or gamma-carboxy Glu; Xaa at residue 11, 26 and 28 is Pro or Hyp; Xaa at residue 31 is Trp or Bromo Trp

<400> 290
 Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Xaa Ser Gln Cys Cys Arg
 1 5 10 15
 Ser Ser Cys Lys Asn Gly Arg Cys Ala Xaa Ser Xaa Xaa Xaa Xaa
 20 25 30

<210> 291
 <211> 372
 <212> DNA
 <213> Conus viola

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<400> 291
accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg      60
acggcctgtc agctcattat agctggggac tccagaggta cgcagttgca tcgtgccctg      120
aggaaggcca ccaaactctc cgtgtcgact cgctgcaaga gtagaggatc atcatgtcgt      180
aggacttcgt atgactgctg cacgggttct tgcagaaatg gtaaattgtg ctgatccagc      240
gcctgatctt ccccttctg tgctccatcc ttttctgcct gagtcctcct tacctgagag      300
tgggcatgaa ccactcatca cctactccct ggaagcttca gaggagctac attgaaataa      360
aagccgcatt gc                                                              372

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<210> 292
<211> 71
<212> PRT
<213> Conus viola

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<400> 292
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1          5          10          15
Cys Gln Leu Ile Ile Ala Gly Asp Ser Arg Gly Thr Gln Leu His Arg
          20          25          30
Ala Leu Arg Lys Ala Thr Lys Leu Ser Val Ser Thr Arg Cys Lys Ser
          35          40          45
Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys Thr Gly Ser
          50          55          60
Cys Arg Asn Gly Lys Cys Gly
65          70

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<210> 293
<211> 25
<212> PRT
<213> Conus viola

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<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
      -sulpho-Tyr or O-phospho-Tyr

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<400> 293
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Xaa Asp Cys Cys
1          5          10          15
Thr Gly Ser Cys Arg Asn Gly Lys Cys
          20          25

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<210> 294
<211> 380
<212> DNA
<213> Conus viola

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<400> 294
accaaaacca tcatcaaaat gaaactgacg tgtgtggcga tcgtcgccgt gctgctcctg      60
acggcctgtc agctcattac agctgaagac tccagaggta cgcagtgagca tcttgccctg      120

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aagtcgacct ccaaagtctc caagtcgact agctgcatgg aagccagatc ttattgcgga 180
 cctgctacta cgaaaatctg ctgcatgttt tgcagtccat tcagcgatag atgtatgaac 240
 aatcccaaca attgatcttc ccccttggtg gctccatctt ttctgcctga gtcctcctta 300
 cctgagagtg gtcatgaacc actcatcacc tactcctctg gaggcttcag aggagttaca 360
 ttgaaataaa agccgcatgc 380

<210> 295
 <211> 78
 <212> PRT
 <213> Conus viola

<400> 295
 Met Lys Leu Thr Cys Val Ala Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr His Glu His Leu
 20 25 30
 Ala Leu Lys Ser Thr Ser Lys Val Ser Lys Ser Thr Ser Cys Met Glu
 35 40 45
 Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr Lys Ile Cys Cys Asp Phe
 50 55 60
 Cys Ser Pro Phe Ser Asp Arg Cys Met Asn Asn Pro Asn Asn
 65 70 75

<210> 296
 <211> 36
 <212> PRT
 <213> Conus viola

<220>
 <221> PEPTIDE
 <222> (1)..(36)
 <223> Xaa at residue6 is Glu or gamma-carboxy Glu; Xaa at residue 13,
 25 and 34 is Pro or Hyp; Xaa at residue 10 is Tyr, 125I-Tyr, mono
 -iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 296
 Ser Thr Ser Cys Met Xaa Ala Arg Ser Xaa Cys Gly Xaa Ala Thr Thr
 1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Xaa Phe Ser Asp Arg Cys Met Asn
 20 25 30
 Asn Xaa Asn Asn
 35

<210> 297
 <211> 373
 <212> DNA
 <213> Conus viola

<400> 297
 accaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgctcctg 60
 acggcctgtc agctcattac agctgaggac tccagaggta cgcagttgca tcgtgccctg 120
 aggaagacca ccaaactctc cttgtcgact cgctgcaagg gtccaggagc catatgtata 180

aggattgcgt ataactgctg caagtattct tgcggaaatg gtaaattgtgg ctgatccagc 240
gcctgatctt ccccttgtg tgctccatcc tttttctgcc tgagtcctcc ttacctgaga 300
gtggatcatga accactcatc acctactcct ctggaggcct cagaggagct acattgaaat 360
aaaagccgca tgc 373

<210> 298
<211> 71
<212> PRT
<213> Conus viola

<400> 298
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Asp Ser Arg Gly Thr Gln Leu His Arg
20 25 30

Ala Leu Arg Lys Thr Thr Lys Leu Ser Leu Ser Thr Arg Cys Lys Gly
35 40 45

Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys Lys Tyr Ser
50 55 60

Cys Gly Asn Gly Lys Cys Gly
65 70

<210> 299
<211> 25
<212> PRT
<213> Conus viola

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa at residue 3 is Pro or Hyp; Xaa at residue 13 and 18 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 299
Cys Lys Gly Xaa Gly Ala Ile Cys Ile Arg Ile Ala Xaa Asn Cys Cys
1 5 10 15

Lys Xaa Ser Cys Gly Asn Gly Lys Cys
20 25

<210> 300
<211> 353
<212> DNA
<213> Conus viola

<400> 300
acaaaaacca tcatcaaaat gaaactgacg tgtgtggtga tcgtcgccgt gctgttcctg 60
acggcctgtc aattcatcac agctgatgac tccagaagta cgcagaagca tcgtgccctg 120
aggtcgacca ccaaactt tatgttgact tggtactgca cgccttatgg aggacattgt 180
ggttattata atgactgctg cagtcacaa tgcaatataa acagaaataa atgtgagtag 240
ctgatccggc atctgatctg tgctcgccct aacctgagag tggatcatgaa ccactcatca 300

tctactcctc tggaggcttc agaggagcta catggaaata aaagccgcat tgc 353

<210> 301

<211> 73

<212> PRT

<213> Conus viola

<400> 301

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Phe Ile Thr Ala Asp Asp Ser Arg Ser Thr Gln Lys His Arg
20 25 30

Ala Leu Arg Ser Thr Thr Lys His Phe Met Leu Thr Trp Tyr Cys Thr
35 40 45

Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys Ser His Gln
50 55 60

Cys Asn Ile Asn Arg Asn Lys Cys Glu
65 70

<210> 302

<211> 28

<212> PRT

<213> Conus viola

<220>

<221> PEPTIDE

<222> (1)..(28)

<223> Xaa at residue 28 is Glu or gamma-carboxy Glu; Xaa at residue 4 is Pro or Hyp; Xaa at residue 1, 5, 11 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 302

Xaa Cys Thr Xaa Xaa Gly Gly His Cys Gly Xaa Xaa Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Xaa
20 25

<210> 303

<211> 294

<212> DNA

<213> Conus pulicarius

<400> 303

ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60

ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120

gacaaaaact ccaagttgac caggggaatgc acacctccag atggagcttg tggtttacct 180

acacactgct gcggggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240

tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 304

<211> 73

<212> PRT

<213> Conus pulicarius

<400> 304

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Arg Glu Cys
35 40 45

Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu
65 70

<210> 305

<211> 27

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5
and 12 is Pro or Hyp

<400> 305

Xaa Cys Thr Xaa Xaa Asp Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 306

<211> 294

<212> DNA

<213> Conus pulicarius

<400> 306

ggatccatga aactgacgtg cgtggtgatt atcgccgtgc tgttcctgac ggcctgtcaa 60

ctcattacag ctgagactta ctccagaggt aagcagatgc accgtgctct gaggtcaact 120

gacaaaaact ccagttgac cagggaatgc acacctccag gtggagcttg tggtttacct 180

acacactgct gcggggttttg cgatatggca aacaacagat gtctgtaaag cgtctgatat 240

tccccttctg tgctctatcc tctttggcct gagtcatcca tacctgtgct cgag 294

<210> 307

<211> 73

<212> PRT

<213> Conus pulicarius

<400> 307

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala
1 5 10 15

Cys Gln Leu Ile Thr Ala Glu Thr Tyr Ser Arg Gly Lys Gln Met His
20 25 30

Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Gln Leu Thr Arg Glu Cys
35 40 45

Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys Gly Phe
 50 55 60

Cys Asp Met Ala Asn Asn Arg Cys Leu
 65 70

<210> 308
 <211> 27
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 1 is Glu or gamma-carboxy Glu; Xaa at residue 4, 5
 and 12 is Pro or Hyp

<400> 308
 Xaa Cys Thr Xaa Xaa Gly Gly Ala Cys Gly Leu Xaa Thr His Cys Cys
 1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
 20 25

<210> 309
 <211> 307
 <212> DNA
 <213> Conus rattus

<400> 309
 ggatccatga aactgacgtg tgtggtgatc atcgccgtgc tgttcctggc agcctgtcaa 60
 cctgttacaa ctgagacttt ctccagaggt aaggagaagc gtcgtgctct gaggtcaact 120
 gacggcaact cccggttgac cagggcatgc acgcctgaag gtggagcctg tagtagtggg 180
 cgtcactgct gcggcttttg cgataacgtg tcccacacgt gctatgggtga aacaccatct 240
 ctccactgat gtttcccctt ctgtgctcta tcttcttttg cctgagtcac ccatacctgt 300
 gctcgag 307

<210> 310
 <211> 80
 <212> PRT
 <213> Conus rattus

<400> 310
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Ala Ala
 1 5 10 15

Cys Gln Pro Val Thr Thr Glu Thr Phe Ser Arg Gly Lys Glu Lys Arg
 20 25 30

Arg Ala Leu Arg Ser Thr Asp Gly Asn Ser Arg Leu Thr Arg Ala Cys
 35 40 45

Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys Gly Phe
 50 55 60

Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser Leu His
 65 70 75 80

<210> 311

<211> 34
 <212> PRT
 <213> Conus rattus

<220>
 <221> PEPTIDE
 <222> (1)..(34)
 <223> Xaa at residue 5 and 29 is Glu or gamma-carboxy Glu; Xaa at residue 4 and 31 is Pro or Hyp; Xaa at residue 27 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 311
 Ala Cys Thr Xaa Xaa Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
 1 5 10 15
 Gly Phe Cys Asp Asn Val Ser His Thr Cys Xaa Gly Xaa Thr Xaa Ser
 20 25 30

Leu His

<210> 312
 <211> 342
 <212> DNA
 <213> Conus stercusmuscarum

<220>
 <221> misc_feature
 <222> (1)..(342)
 <223> n may be any nucleotide

<400> 312
 agatccatga aactgacgtg cgtgggtgatc gtcgccgtgc tgctcctgac ggcctgtcaa 60
 ctcatcacag ctgatgactc cagaggtacg caggagcatc gtgccctgag gtcggacacc 120
 aaactcccca tatcgactcg ctgcaagggt aaaggagcat catgtcataa gactatgtat 180
 gactgctgca gcggttcttg caccagaggt agatgtggct gatccagcgc ctgatcttcc 240
 cccttctgtg ctctatcctt ttctgcctga gtcatacatc ctgtgctcga gcgttactag 300
 tggatccgag ctcggtacca agcttggcgt aatcataaaa nc 342

<210> 313
 <211> 71
 <212> PRT
 <213> Conus stercusmuscarum

<400> 313
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Leu Leu Thr Ala
 1 5 10 15
 Cys Gln Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Glu His Arg
 20 25 30
 Ala Leu Arg Ser Asp Thr Lys Leu Pro Ile Ser Thr Arg Cys Lys Gly
 35 40 45
 Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys Ser Gly Ser
 50 55 60
 Cys Thr Arg Gly Arg Cys Gly
 65 70

<210> 314
 <211> 25
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(25)
 <223> Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 314
 Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Xaa Asp Cys Cys
 1 5 10 15

~~Ser Gly Ser Cys Thr Arg Gly Arg Cys~~
~~20 25~~

<210> 315
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 315
 Gln Cys Ser Ala Asn Gly Gly Ser Cys Thr Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Asp Ser Ser Val Cys Val Ala Thr Ser Tyr
 20 25 30

Pro

<210> 316
 <211> 28
 <212> PRT
 <213> Conus arenatus

<400> 316
 Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Arg His Cys Cys
 1 5 10 15

Ser Gly Tyr Cys His Lys Thr Ile Gln Ala Cys Ser
 20 25

<210> 317
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 317
 Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
 1 5 10 15

Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
 20 25 30

Pro

<210> 318
 <211> 33
 <212> PRT
 <213> Conus arenatus

<400> 318

Gln Cys Thr Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15

Ser Leu Tyr Cys Asn Lys Ser Thr Gly Val Cys Ile Ala Thr Ser Tyr
20 25 30

Pro

<210> 319

<211> 27

<212> PRT

<213> Conus arenatus

<400> 319

Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Thr Ala Asn Asn Arg Cys Leu
20 25

<210> 320

<211> 28

<212> PRT

<213> Conus arenatus

<400> 320

Thr Cys Asn Thr Pro Thr Glu Tyr Cys Thr Leu His Gln His Cys Cys
1 5 10 15

Ser Gly His Cys His Lys Thr Ile Gln Ala Cys Ala
20 25

<210> 321

<211> 30

<212> PRT

<213> Conus arenatus

<400> 321

Gln Cys Ser Pro Ile Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
1 5 10 15

Ser Asn His Cys Ile Lys Pro Ile Gly Arg Cys Val Ala Thr
20 25 30

<210> 322

<211> 30

<212> PRT

<213> Conus arenatus

<400> 322

Gln Cys Leu Pro Asn Gly Gly Tyr Cys Thr Leu His Ile His Cys Cys
1 5 10 15

Ser Asp His Cys Ile Lys Pro Ile Asp Arg Cys Val Ala Thr
20 25 30

<210> 323

<211> 25

<212> PRT

<213> Conus aurisiacus

<400> 323

Cys Lys Gly Lys Gly Lys Pro Cys Ser Arg Ile Ser Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 324
<211> 32
<212> PRT
<213> Conus aurisiacus

<400> 324
Cys Met Glu Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg Ile Cys Cys
1 5 10 15

Gly Phe Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr Pro Ser Asn
20 25 30

<210> 325
<211> 25
<212> PRT
<213> Conus aurisiacus

<400> 325
Cys Lys Ala Lys Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 326
<211> 26
<212> PRT
<213> Conus aurisiacus

<400> 326
Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Pro Gly Arg Asn Ile Cys Thr
20 25

<210> 327
<211> 36
<212> PRT
<213> Conus bullatus

<400> 327
Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
1 5 10 15

Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
20 25 30

Asn Pro Asn Asn
35

<210> 328
<211> 31
<212> PRT
<213> Conus bullatus

<400> 328
Cys Ile Thr Pro Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
1 5 10 15

Gly Pro Cys Lys Asn Gly Arg Cys Thr Pro Ser Pro Ser Glu Trp

20

25

30

<210> 329
 <211> 26
 <212> PRT
 <213> Conus bullatus

<400> 329
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Pro Ala Arg Arg Thr Cys Thr
 20 25

<210> 330
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 330
 Cys Lys Gly Pro Gly Ala Ser Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Lys Tyr Ser Cys Arg Asn Gly Lys Cys
 20 25

<210> 331
 <211> 36
 <212> PRT
 <213> Conus bullatus

<400> 331
 Ser Thr Ser Cys Met Ala Ala Gly Ser Tyr Cys Gly Pro Ala Thr Thr
 1 5 10 15
 Asn Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Lys
 20 25 30
 Lys Pro Asn Asn
 35

<210> 332
 <211> 25
 <212> PRT
 <213> Conus bullatus

<400> 332
 Cys Lys Ser Lys Gly Ser Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Asn Gly Arg Cys
 20 25

<210> 333
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 333
 Cys Lys Ser Thr Gly Ala Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Arg Cys
 20 25

<210> 334
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 334
 Cys Gln Gly Arg Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Asn Arg Gly Ser Cys
 20 25

<210> 335
 <211> 28
 <212> PRT
 <213> Conus catus

<400> 335
 Cys Leu Pro Ala Gly Glu Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
 1 5 10 15
 Gly Thr Cys Ser Ser Val Leu Lys Ser Cys Val Ser
 20 25

<210> 336
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 336
 Cys Gln Gly Arg Gly Gly Pro Cys Thr Lys Ala Val Phe Asn Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 337
 <211> 26
 <212> PRT
 <213> Conus catus

<400> 337
 Cys Ala Thr Tyr Gly Lys Pro Cys Gly Ile Gln Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 338
 <211> 25
 <212> PRT
 <213> Conus catus

<400> 338
 Cys Arg Gly Arg Gly Gly Pro Cys Thr Lys Ala Met Phe Asn Cys Cys
 1 5 10 15
 Ser Gly Ser Cys Asn Arg Gly Arg Cys
 20 25

<210> 339
 <211> 33
 <212> PRT
 <213> Conus characteristicus

<400> 339

Gln	Cys	Ser	Ala	Asn	Gly	Gly	Ser	Cys	Thr	Arg	His	Phe	His	Cys	Cys
1				5					10					15	

Ser	Leu	Tyr	Cys	Asn	Lys	Asp	Ser	Ser	Val	Cys	Val	Ala	Thr	Ser	Tyr
			20					25					30		

Pro

<210> 340

<211> 26

<212> PRT

<213> Conus consors

<400> 340

Cys	Ala	Ser	Tyr	Gly	Lys	Pro	Cys	Gly	Ile	Asp	Asn	Asp	Cys	Cys	Asn
1				5					10					15	

Thr	Cys	Asp	Pro	Ala	Arg	Lys	Thr	Cys	Thr
			20					25	

<210> 341

<211> 25

<212> PRT

<213> Conus consors

<400> 341

Cys	Lys	Gly	Thr	Gly	Lys	Pro	Cys	Ser	Arg	Ile	Ala	Tyr	Asn	Cys	Cys
1				5					10					15	

Thr	Gly	Ser	Cys	Arg	Ser	Gly	Lys	Cys
			20					25

<210> 342

<211> 36

<212> PRT

<213> Conus consors

<400> 342

Ala	Thr	Asp	Cys	Ile	Glu	Ala	Gly	Asn	Tyr	Cys	Gly	Pro	Thr	Val	Met
1				5					10					15	

Lys	Ile	Cys	Cys	Gly	Phe	Cys	Ser	Pro	Tyr	Ser	Lys	Ile	Cys	Met	Asn
			20					25					30		

Tyr	Pro	Gln	Asn
			35

<210> 343

<211> 27

<212> PRT

<213> Conus catus

<400> 343

Cys	Lys	Gly	Lys	Gly	Ala	Ser	Cys	Thr	Arg	Leu	Met	Tyr	Asp	Cys	Cys
1				5					10					15	

His	Gly	Ser	Cys	Ser	Ser	Ser	Lys	Gly	Arg	Cys
			20					25		

<210> 344

<211> 25

<212> PRT

<213> Conus consors

<400> 344

Cys Lys Gly Lys Gly Ala Ser Cys His Arg Thr Ser Tyr Asp Cys Cys
 1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
 20 25

<210> 345

<211> 26

<212> PRT

<213> Conus consors

<400> 345

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 5 10 15

Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 346

<211> 25

<212> PRT

<213> Conus consors

<400> 346

Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Val Ala Tyr Asn Cys Cys
 1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 347

<211> 35

<212> PRT

<213> Conus consors

<400> 347

Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
 1 5 10 15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Phe Cys Ile Asp Phe
 20 25 30

Pro Ser Asn
 35

<210> 348

<211> 25

<212> PRT

<213> Conus circumcisis

<400> 348

Cys Lys Gly Lys Gly Ala Ser Cys Arg Lys Thr Met Tyr Asn Cys Cys
 1 5 10 15

Ser Gly Ser Cys Ser Asn Gly Arg Cys
 20 25

<210> 349

<211> 35

<212> PRT

<213> Conus circumcisis

<400> 349

Ser Thr Ser Cys Met Glu Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
1 5 10 15

Thr Cys Cys Gly Tyr Cys Ser Tyr Phe Ser Lys Lys Cys Ile Asp Phe
20 25 30

Pro Ser Asn
35

<210> 350
<211> 27
<212> PRT
<213> Conus circumciscus

<400> 350
Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Ser Arg Tyr Ser Gly Arg Cys
20 25

<210> 351
<211> 35
<212> PRT
<213> Conus circumciscus

<400> 351
Ser Thr Gly Cys Met Lys Ala Gly Ser Tyr Cys Arg Ser Thr Thr Arg
1 5 10 15

Thr Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
20 25 30

Pro Ser Asn
35

<210> 352
<211> 28
<212> PRT
<213> Conus dalli

<400> 352
Ser Cys Thr Pro Pro Gly Gly Pro Cys Gly Tyr Tyr Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Ser Arg Asn Lys Cys Glu
20 25

<210> 353
<211> 25
<212> PRT
<213> Conus distans

<220>
<221> PEPTIDE
<222> (1)..(25)
<223> Xaa is Hyp

<400> 353
Cys Glu Asp Xaa Gly Glu Xaa Cys Gly Ser Asp His Ser Cys Cys Gly
1 5 10 15

Gly Ser Cys Asn His Asn Val Cys Ala
20 25

<210> 354
 <211> 27
 <212> PRT
 <213> Conus ermineus

<400> 354
 Pro Cys Lys Pro Lys Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
 1 5 10 15
 Cys Asn Lys Thr Cys Thr Arg Ser Lys Cys Pro
 20 25

<210> 355
 <211> 27
 <212> PRT
 <213> Conus ermineus

<400> 355
 Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
 1 5 10 15
 Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
 20 25

<210> 356
 <211> 27
 <212> PRT
 <213> Conus geographus

<400> 356
 Cys Lys Ser Pro Gly Ser Ser Cys Ser Pro Thr Ser Tyr Asn Cys Cys
 1 5 10 15
 Arg Ser Cys Asn Pro Tyr Ala Lys Arg Cys Tyr
 20 25

<210> 357
 <211> 29
 <212> PRT
 <213> Conus geographus

<400> 357
 Cys Lys Ser Pro Gly Thr Pro Cys Ser Arg Gly Met Arg Asp Cys Cys
 1 5 10 15
 Thr Pro Cys Leu Leu Tyr Ser Asn Lys Cys Arg Arg Tyr
 20 25

<210> 358
 <211> 30
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 358
 Cys Leu Ser Pro Gly Ser Arg Cys His Lys Thr Met Arg Asn Cys Cys
 1 5 10 15
 Thr Ser Cys Ser Ser Tyr Lys Gly Lys Cys Arg Pro Arg Lys
 20 25 30

<210> 359

<211> 27
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 359
 Cys Lys Pro Pro Gly Arg Lys Cys Leu Asn Arg Lys Asn Glu Cys Cys
 1 5 10 15
 Ser Lys Phe Cys Asn Glu His Leu His Met Cys
 20 25

<210> 360
 <211> 26
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 360
 Cys Lys Pro Pro Arg Arg Lys Cys Leu Lys Ile Lys Asp Lys Cys Cys
 1 5 10 15
 Asn Phe Cys Asn Thr His Leu Asn Met Cys
 20 25

<210> 361
 <211> 28
 <212> PRT
 <213> Unknown

<220>
 <223> unknown Conus species

<400> 361
 Cys Ala Gly Pro Gly Thr Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
 1 5 10 15
 Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
 20 25

<210> 362
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<400> 362
 Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15
 Ser Gly Cys Asp Arg Asn Arg Asn Lys Cys Tyr
 20 25

<210> 363
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<400> 363
 Cys Leu Pro Pro Gly Ser Tyr Cys Lys Ala Thr Thr Glu Val Cys Cys
 1 5 10 15

Ser Ser Cys Leu Gln Phe Ala Gln Ile Cys Ser
20 25

<210> 364
<211> 30
<212> PRT
<213> Conus lynceus

<400> 364
Cys Lys Ser Pro Gly Ser Pro Cys Ser Val Thr Ser Tyr Asn Cys Cys
1 5 10 15

Thr Phe Cys Ser Ser Tyr Thr Lys Lys Cys Arg Ala Ser Leu
20 25 30

<210> 365
<211> 28
<212> PRT
<213> Conus lynceus

<400> 365
Cys Ala Gly Pro Gly Ala Ile Cys Pro Asn Arg Val Cys Cys Gly Tyr
1 5 10 15

Cys Ser Lys Arg Thr His Leu Cys His Ser Arg Thr
20 25

<210> 366
<211> 27
<212> PRT
<213> Conus lynceus

<400> 366
Ala Cys Trp Ser Ser Gly Thr Pro Cys Gly Thr Asp Ser Leu Cys Cys
1 5 10 15

Gly Gly Cys Asn Val Ser Lys Ser Lys Cys Asn
20 25

<210> 367
<211> 27
<212> PRT
<213> Conus lynceus

<400> 367
Lys Cys Trp Ser Pro Gly Thr Tyr Cys Arg Ala His Ser Lys Cys Cys
1 5 10 15

Arg Gly Cys Asp Gln Asn Arg Asn Lys Cys Tyr
20 25

<210> 368
<211> 29
<212> PRT
<213> Conus laterculatus

<400> 368
Cys Lys Ser Pro Gly Ser Ser Cys Ser Val Ser Met Arg Asn Cys Cys
1 5 10 15

Thr Ser Cys Asn Ser Arg Thr Lys Lys Cys Thr Arg Arg
20 25

<210> 369

<211> 27
 <212> PRT
 <213> Conus laterculatus

<400> 369
 Thr Cys Trp Pro Ser Gly Thr Ala Cys Gly Ile Asp Ser Asn Cys Cys
 1 5 10 15
 Ser Gly Cys Asn Val Ser Arg Ser Lys Cys Asn
 20 25

<210> 370
 <211> 27
 <212> PRT
 <213> Conus laterculatus

<400> 370
 Lys Cys Trp Pro Ser Gly Ser Tyr Cys Arg Ala Asn Ser Lys Cys Cys
 1 5 10 15
 Ser Gly Cys Asp Arg Asn Arg Ser Lys Cys Asn
 20 25

<210> 371
 <211> 37
 <212> PRT
 <213> Conus leopardus

<400> 371
 Ser Leu Phe Glu Cys Ala Pro Ser Gly Gly Arg Cys Gly Phe Leu Lys
 1 5 10 15
 Ser Cys Cys Glu Gly Tyr Cys Asp Gly Glu Ser Thr Ser Cys Val Ser
 20 25 30
 Gly Pro Tyr Ser Ile
 35

<210> 372
 <211> 30
 <212> PRT
 <213> Conus leopardus

<400> 372
 Trp Pro Leu Asp Cys Thr Ala Pro Ser Gln Pro Cys Gly Tyr Phe Pro
 1 5 10 15
 Arg Cys Cys Gly His Cys Asp Val Arg Arg Val Cys Thr Ser
 20 25 30

<210> 373
 <211> 31
 <212> PRT
 <213> Conus leopardus

<400> 373
 Cys Met Ser Pro Gly Gly Ile Cys Gly Asp Phe Gly Asp Cys Cys Glu
 1 5 10 15
 Ile Cys Asn Val Tyr Gly Ile Cys Val Ser Asp Leu Pro Gly Ile
 20 25 30

<210> 374
 <211> 27

<212> PRT
 <213> Conus leopardus

<400> 374
 Tyr Cys Ala Pro Pro Gly Gly Ala Cys Gly Phe Phe Asp His Cys Cys
 1 5 10 15
 Gly Tyr Cys Glu Thr Phe Tyr Asn Thr Cys Arg
 20 25

<210> 375
 <211> 25
 <212> PRT
 <213> Conus magus

<400> 375
 Cys Lys Gly Thr Gly Lys Pro Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 376
 <211> 26
 <212> PRT
 <213> Conus magus

<400> 376
 Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
 1 5 10 15
 Thr Cys Asp Pro Ala Arg Lys Thr Cys Thr
 20 25

<210> 377
 <211> 27
 <212> PRT
 <213> Conus miles

<400> 377
 Cys Asn Asp Arg Gly Gly Gly Cys Ser Gln His Pro His Cys Cys Gly
 1 5 10 15
 Gly Thr Cys Asn Lys Leu Ile Gly Val Cys Leu
 20 25

<210> 378
 <211> 25
 <212> PRT
 <213> Conus monachus

<400> 378
 Cys Lys Ser Thr Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15
 Thr Gly Ser Cys Arg Ser Gly Lys Cys
 20 25

<210> 379
 <211> 25
 <212> PRT
 <213> Conus monachus

<400> 379

Cys Lys Gly Lys Gly Ser Ser Cys Ser Arg Thr Met Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Lys Cys
20 25

<210> 380
<211> 35
<212> PRT
<213> Conus obscurus

<400> 380
Ser Pro Pro Cys Met Lys Gly Gly Ser Ser Cys Arg Gly Thr Thr Gly
1 5 10 15

Val Cys Cys Gly Phe Cys Ser Asp Phe Gly Tyr Lys Cys Arg Asp Tyr
20 25 30

Pro Gln Asn
35

<210> 381
<211> 28
<212> PRT
<213> Conus obscurus

<400> 381
Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys
1 5 10 15

Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser
20 25

<210> 382
<211> 27
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa is Hyp

<400> 382
Xaa Cys Lys Thr Xaa Gly Arg Lys Cys Phe Xaa His Gln Lys Asp Cys
1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
20 25

<210> 383
<211> 26
<212> PRT
<213> Conus purpurascens

<220>
<221> PEPTIDE
<222> (1)..(26)
<223> Xaa at residue 5 is Hyp; Xaa at residue 12 is gamma-carboxy-Glu

<400> 383
Ser Cys Lys Leu Xaa Gly Ala Tyr Cys Asn Ala Xaa Asp Tyr Asp Cys
1 5 10 15

Cys Leu Arg Cys Lys Val Gly Gly Thr Cys
20 25

<210> 384
<211> 27
<212> PRT
<213> Conus purpurascens

<400> 384
Pro Cys Lys Lys Thr Gly Arg Lys Cys Phe Pro His Gln Lys Asp Cys
1 5 10 15

Cys Gly Arg Ala Cys Ile Ile Thr Ile Cys Pro
20 25

<210> 385
<211> 30
<212> PRT
<213> Conus pulicarius

<400> 385
Gln Cys Ser Pro Asn Gly Gly Ser Cys Ser Arg His Phe His Cys Cys
1 5 10 15

Ser Leu Tyr Cys Asn Lys Asn Thr Gly Val Cys Ile Ala Thr
20 25 30

<210> 386
<211> 27
<212> PRT
<213> Conus pulicarius

<400> 386
Glu Cys Thr Pro Pro Asp Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 387
<211> 27
<212> PRT
<213> Conus pulicarius

<400> 387
Glu Cys Thr Pro Pro Gly Gly Ala Cys Gly Leu Pro Thr His Cys Cys
1 5 10 15

Gly Phe Cys Asp Met Ala Asn Asn Arg Cys Leu
20 25

<210> 388
<211> 28
<212> PRT
<213> Conus radiatus

<400> 388
His Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
1 5 10 15

Cys Ser Lys Phe Cys Asn Ser Val Arg Lys Gln Cys
20 25

<210> 389

<211> 28
 <212> PRT
 <213> Conus radiatus

<400> 389
 Arg Gly Cys Lys Pro Leu Lys Arg Arg Cys Phe Asn Asp Lys Glu Cys
 1 5 10 15
 Cys Ser Lys Phe Cys Asn Ser Val Arg Asn Gln Cys
 20 25

<210> 390
 <211> 27
 <212> PRT
 <213> Conus rattus

<400> 390
 Cys Asn Ala Arg Asn Asp Gly Cys Ser Gln His Ser Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 391
 <211> 27
 <212> PRT
 <213> Conus rattus

<400> 391
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Ala Gly Val Cys Leu
 20 25

<210> 392
 <211> 27
 <212> PRT
 <213> Conus rattus

<400> 392
 Cys Asn Ala Arg Asn Ser Gly Cys Ser Gln His Pro Gln Cys Cys Ser
 1 5 10 15
 Gly Ser Cys Asn Lys Thr Leu Gly Val Cys Leu
 20 25

<210> 393
 <211> 34
 <212> PRT
 <213> Conus rattus

<400> 393
 Ala Cys Thr Pro Glu Gly Gly Ala Cys Ser Ser Gly Arg His Cys Cys
 1 5 10 15
 Gly Phe Cys Asp Asn Val Ser His Thr Cys Tyr Gly Glu Thr Pro Ser
 20 25 30

Leu His

<210> 394
 <211> 36
 <212> PRT

<213> Conus striatus

<400> 394

Ala Thr Asp Cys Ile Glu Ala Gly Asn Tyr Cys Gly Pro Thr Val Met
1 5 10 15

Lys Ile Cys Cys Gly Phe Cys Ser Pro Tyr Ser Lys Ile Cys Met Asn
20 25 30

Tyr Pro Lys Asn
35

<210> 395

<211> 26

<212> PRT

<213> Conus striatus

<400> 395

Cys Lys Leu Lys Gly Gln Ser Cys Arg Arg Thr Met Tyr Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Gly Arg Arg Gly Lys Cys
20 25

<210> 396

<211> 25

<212> PRT

<213> Conus striatus

<400> 396

Cys Lys Ala Ala Gly Lys Ser Cys Ser Arg Ile Ala Tyr Asn Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Ser Gly Lys Cys
20 25

<210> 397

<211> 26

<212> PRT

<213> Conus striatus

<400> 397

Cys Glu Ser Tyr Gly Lys Pro Cys Gly Ile Tyr Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Pro Ala Lys Lys Thr Cys Thr
20 25

<210> 398

<211> 27

<212> PRT

<213> Conus stercusmuscarum

<400> 398

Cys Lys Ser Lys Gly Ala Lys Cys Ser Arg Leu Met Tyr Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Ser Gly Tyr Thr Gly Arg Cys
20 25

<210> 399

<211> 35

<212> PRT

<213> Conus stercusmuscarum

<400> 399

Thr Thr Ser Cys Met Gln Ala Gly Ser Tyr Cys Gly Ser Thr Thr Arg
1 5 10 15

Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Lys Cys Ile Asp Tyr
20 25 30

Pro Ser Asn
35

<210> 400

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<400> 400

Cys Ala Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
20 25

<210> 401

<211> 26

<212> PRT

<213> Conus stercusmuscarum

<400> 401

Cys Val Ser Tyr Gly Lys Pro Cys Gly Ile Asp Asn Asp Cys Cys Asn
1 5 10 15

Ala Cys Asp Pro Ala Arg Asn Ile Cys Thr
20 25

<210> 402

<211> 25

<212> PRT

<213> Conus stercusmuscarum

<400> 402

Cys Lys Gly Lys Gly Ala Ser Cys His Lys Thr Met Tyr Asp Cys Cys
1 5 10 15

Ser Gly Ser Cys Thr Arg Gly Arg Cys
20 25

<210> 403

<211> 25

<212> PRT

<213> Conus striolatus

<400> 403

Cys Lys Gly Lys Gly Ala Ser Cys Leu Arg Thr Ala Tyr Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Asn Arg Gly Arg Cys
20 25

<210> 404

<211> 24

<212> PRT

<213> Conus striolatus

<400> 404

Cys Arg Pro Ser Gly Ser Asn Cys Gly Asn Ile Ser Ile Cys Cys Gly
1 5 10 15

Arg Cys Val Asn Arg Arg Cys Thr
20

<210> 405
<211> 35
<212> PRT
<213> Conus striolatus

<400> 405
Ser Thr Ser Cys Met Lys Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg
1 5 10 15

Ile Cys Cys Gly Tyr Cys Ala Tyr Phe Gly Lys Ile Cys Ile Asp Tyr
20 25 30

Pro Lys Asn
35

<210> 406
<211> 28
<212> PRT
<213> Conus textile

<400> 406
Tyr Cys Thr Pro His Gly Gly His Cys Gly Tyr His Asn Asp Cys Cys
1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
20 25

<210> 407
<211> 31
<212> PRT
<213> Conus viola

<400> 407
Cys Ile Thr Leu Gly Thr Arg Cys Lys Val Pro Ser Gln Cys Cys Arg
1 5 10 15

Ser Ser Cys Lys Asn Gly Arg Cys Ala Pro Ser Pro Glu Glu Trp
20 25 30

<210> 408
<211> 25
<212> PRT
<213> Conus viola

<400> 408
Cys Lys Ser Arg Gly Ser Ser Cys Arg Arg Thr Ser Tyr Asp Cys Cys
1 5 10 15

Thr Gly Ser Cys Arg Asn Gly Lys Cys
20 25

<210> 409
<211> 36
<212> PRT
<213> Conus viola

<400> 409
Ser Thr Ser Cys Met Glu Ala Arg Ser Tyr Cys Gly Pro Ala Thr Thr

1 5 10 15
 Lys Ile Cys Cys Asp Phe Cys Ser Pro Phe Ser Asp Arg Cys Met Asn
 20 25 30

Asn Pro Asn Asn
 35

<210> 410
 <211> 25
 <212> PRT
 <213> Conus viola

<400> 410
 Cys Lys Gly Pro Gly Ala Ile Cys Ile Arg Ile Ala Tyr Asn Cys Cys
 1 5 10 15

Lys Tyr Ser Cys Gly Asn Gly Lys Cys
 20 25

<210> 411
 <211> 28
 <212> PRT
 <213> Conus viola

<400> 411
 Tyr Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Tyr Asn Asp Cys Cys
 1 5 10 15

Ser His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 412
 <211> 27
 <212> PRT
 <213> Conus textile

<400> 412
 Cys Thr Pro Tyr Gly Gly His Cys Gly Tyr Asn His Asp Cys Cys Ser
 1 5 10 15

His Gln Cys Asn Ile Asn Arg Asn Lys Cys Glu
 20 25

<210> 413
 <211> 26
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa is Hyp

<400> 413
 Cys Lys Ser Trp Gly Ser Xaa Cys Ser Xaa Thr Ser Thr Asn Cys Cys
 1 5 10 15

Trp Ser Cys Ser Pro Tyr Arg Lys Lys Cys
 20 25